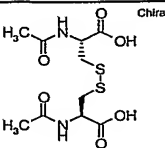
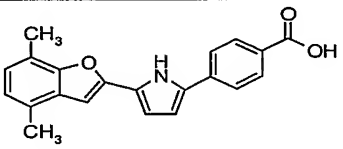
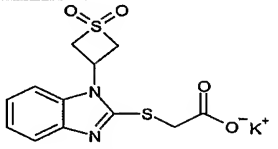
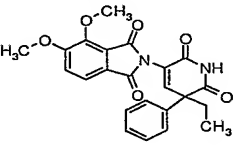
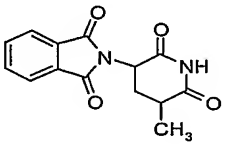
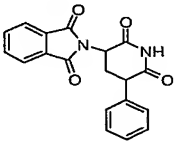
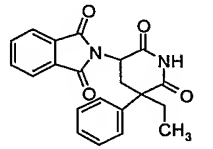
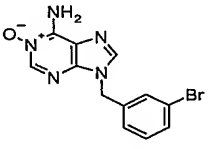
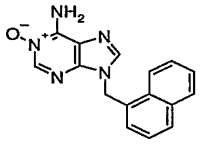
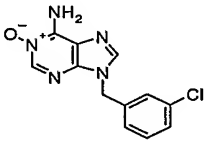
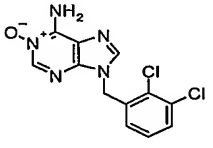
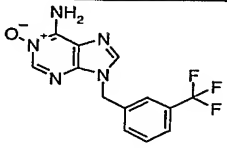
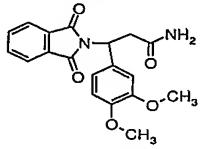
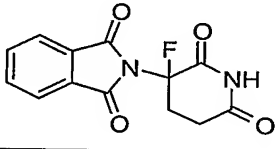
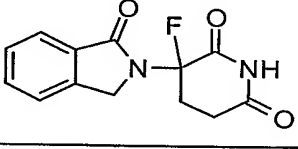
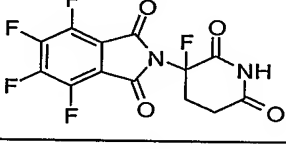
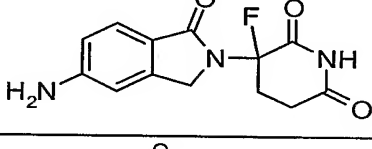
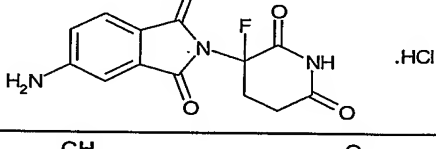
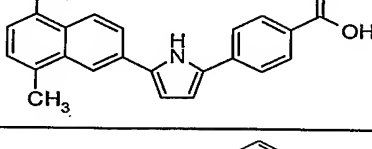
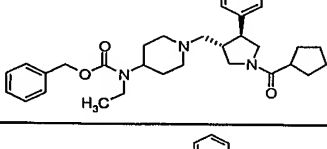
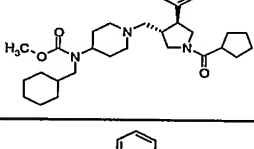
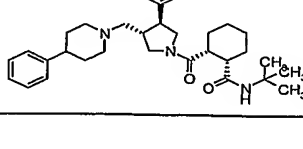
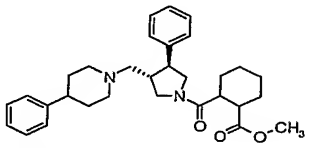
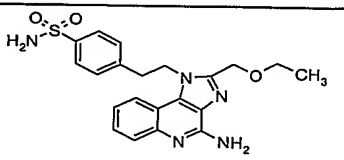
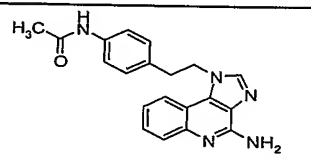
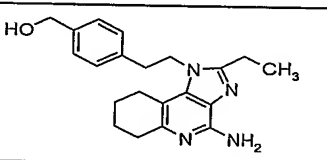
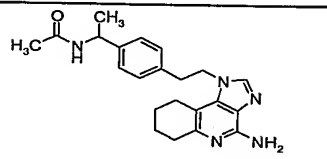
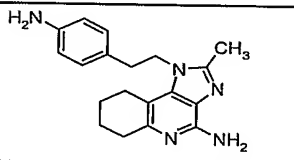
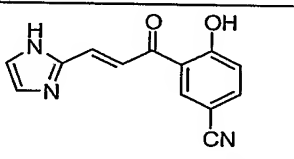
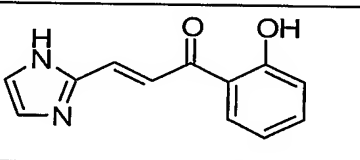
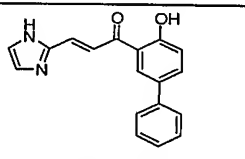
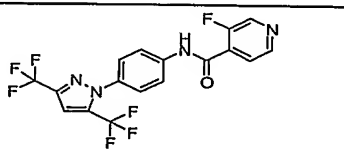
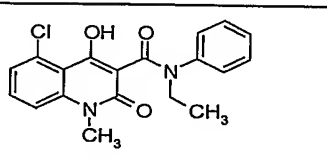
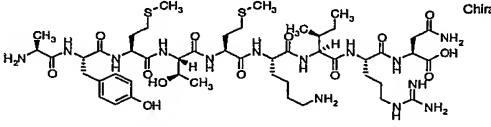
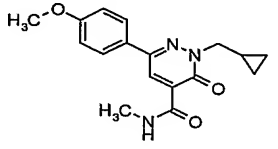
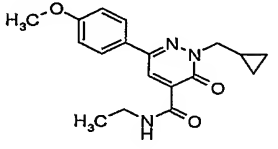
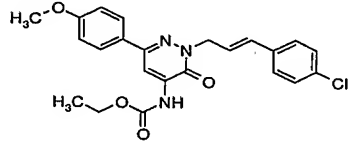
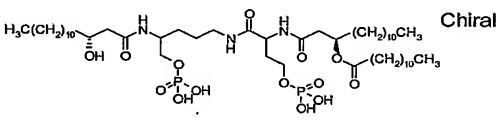
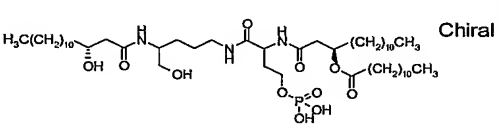
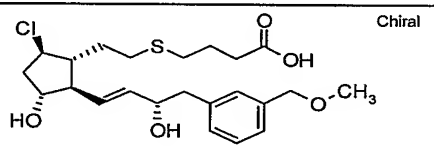
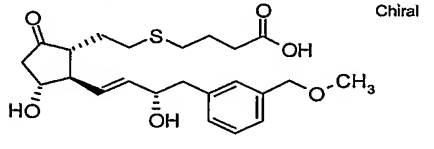
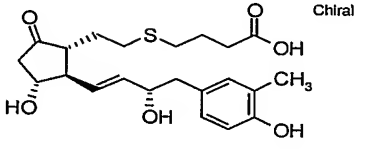
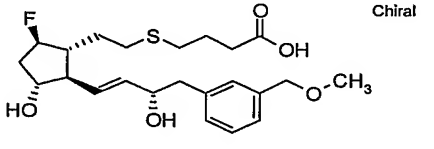
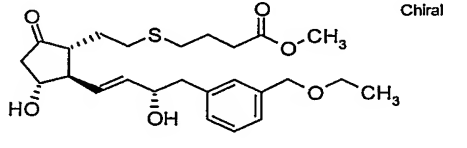
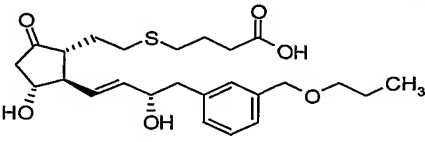
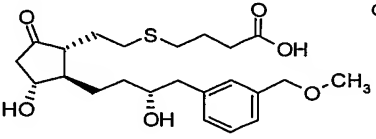
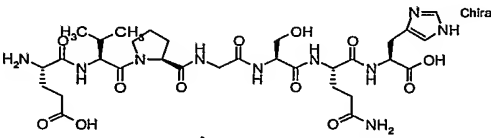
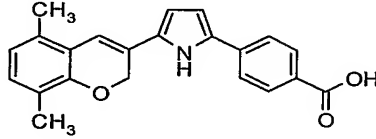
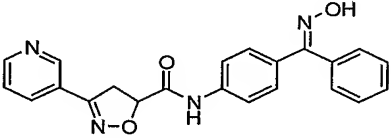
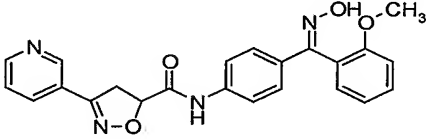
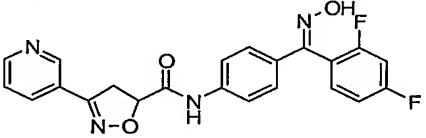
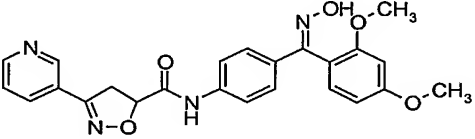
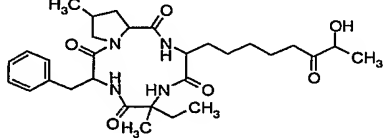
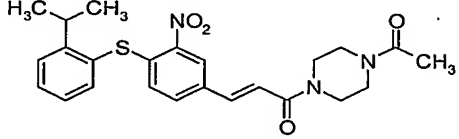
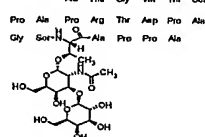


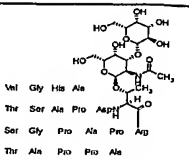
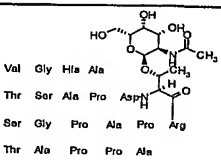
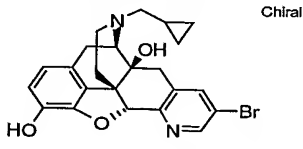
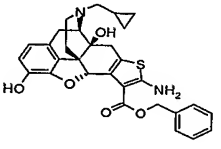
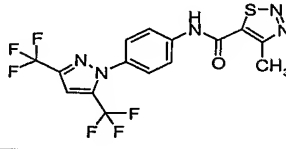
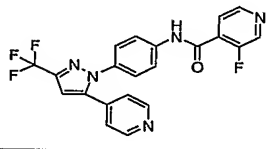
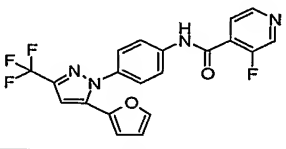
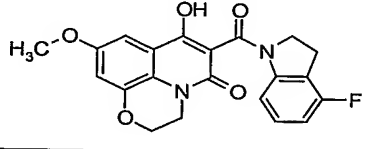
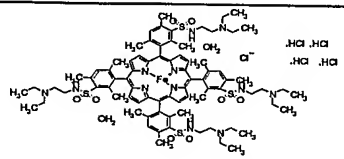
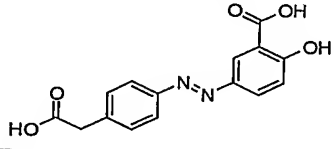
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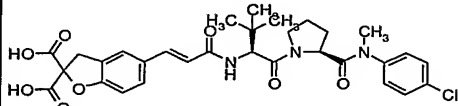
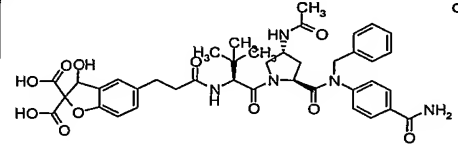
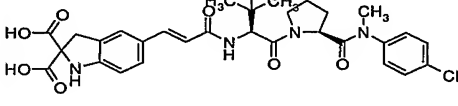
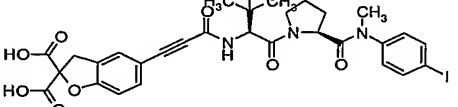
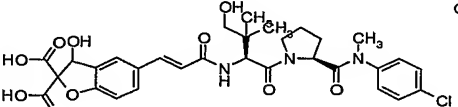
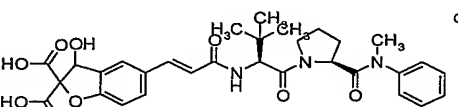
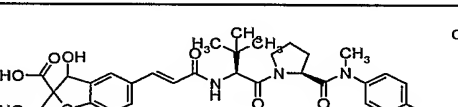
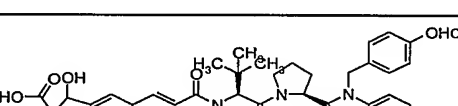
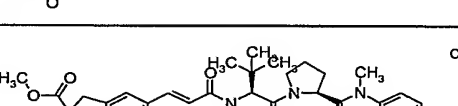
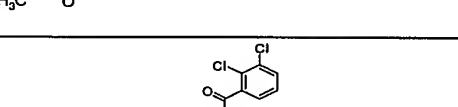
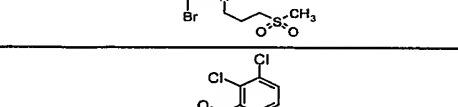
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| 1157 |  Chiral | University of Bristol | | WO 0014114 |
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| 1165 |  Ala His Gly Val Thr Ser Pro Ala Pro Arg Thr Asp Pro Ala Gly Ser-His-Ala Pro Pro Ala | Cancer Research UK | | WO 0052046 |

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| 1166 |  <p>Val Gly His Ala Thr Ser Ala Pro Asp NH Ser Gly Pro Ala Pro Arg Thr Ala Pro Pro Ala</p> | Cancer Research UK | WO 0052046 |
| 1167 |  <p>Val Gly His Ala Thr Ser Ala Pro Asp NH Ser Gly Pro Ala Pro Arg Thr Ala Pro Pro Ala</p> | Cancer Research UK | WO 0052046 |
| 1168 |  <p>Chiral</p> | Southern Research Institute | WO 0112197 |
| 1169 |  <p>Chiral</p> | Southern Research Institute | WO 0112197 |
| 1170 |  | Abbott Labs. | EP 1068187 |
| 1171 |  | Abbott | EP 1068187 |
| 1172 |  | Abbott | EP 1068187 |
| 1173 |  | Fujisawa | Spears, G. et al. 21st Symp Med Chem (Nov 28-30, Kyoto) 2001, Abst 2P-29. |
| 1174 | <p>Val His Phe Phe Arg Asn Ile Pro Thr Arg Ala Thr Val</p> | Austin Research Institute | Tsellos, T. et al. J Med Chem 2002, 45(2): 275. |
| 1175 |  | Eukarion | WO 0204454 |
| 1176 |  | Nobex | 1) Riggs-Sauthier, J.A. et al. 224th ACS Natl Meet (Aug 18-22, Boston) 2002, Abst MEDI 305. |

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| 1177 |  | Tularik | WO 0238107 |
| 1178 |  | Tularik | WO 0238107 |
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| 1186 |  | Sanofi-Synthelabo | WO 0242269 |
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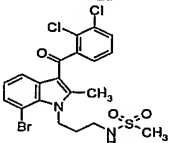
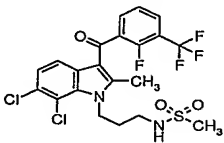
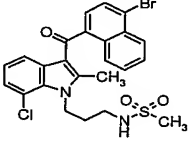
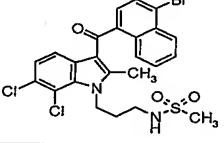
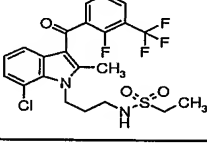
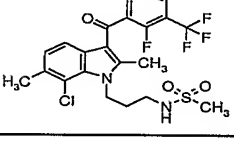
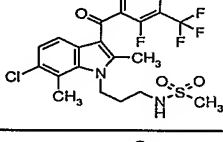
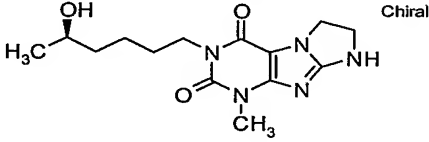
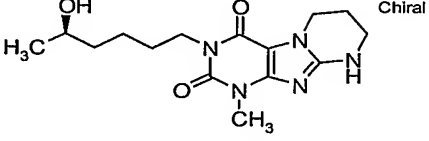
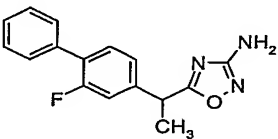
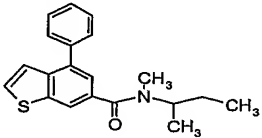
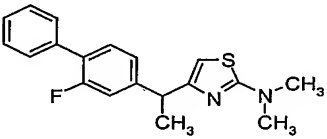
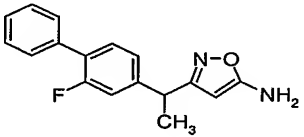
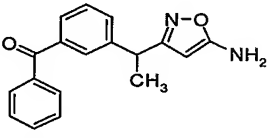
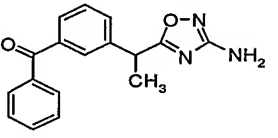
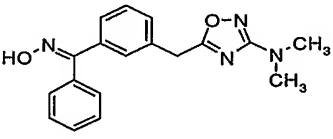
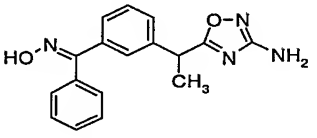
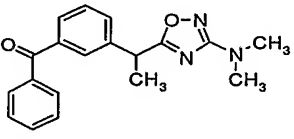
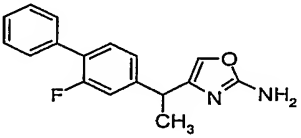
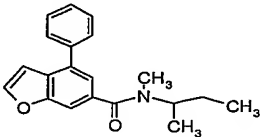
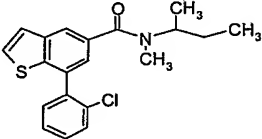
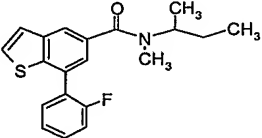
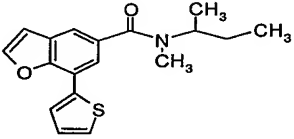
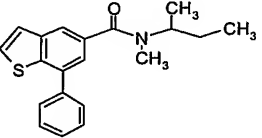
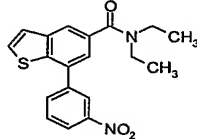
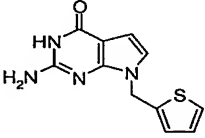
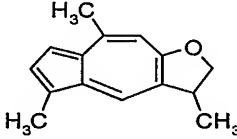
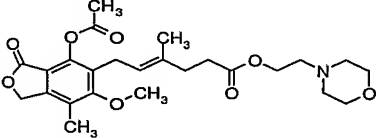
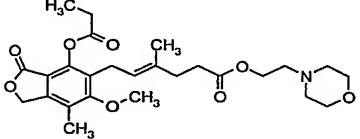
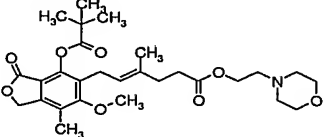
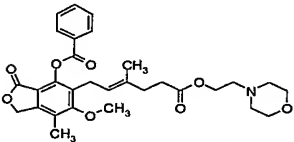
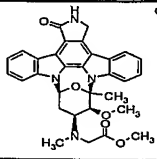
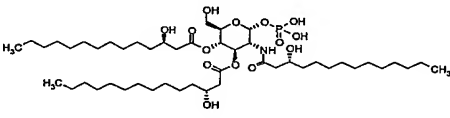
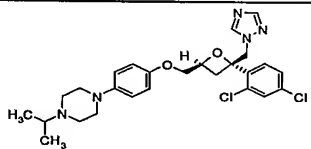
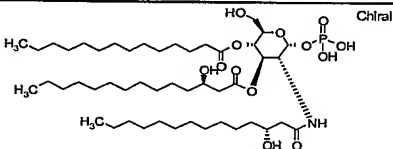
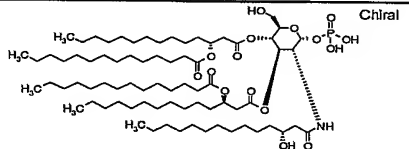
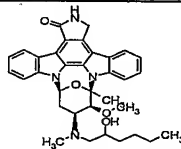
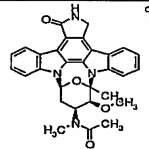
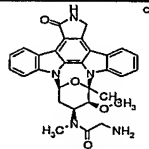
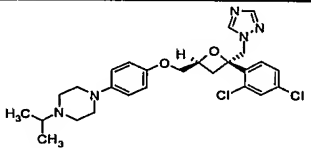
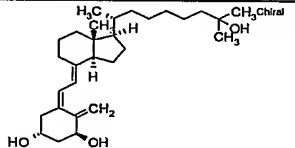
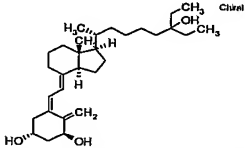
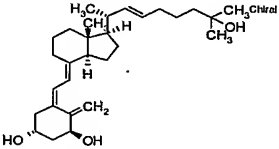
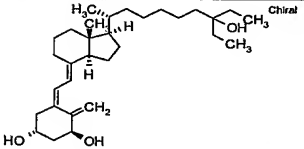
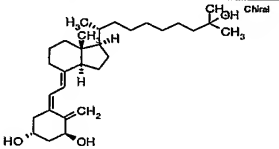
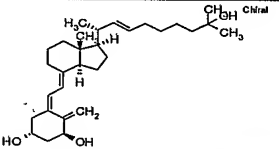
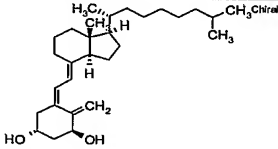
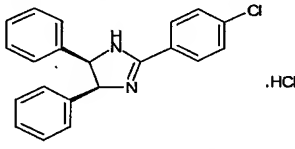
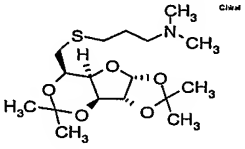
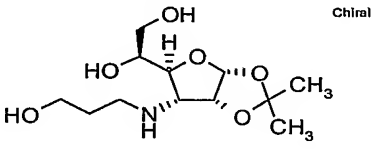
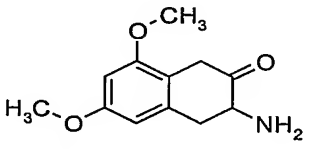
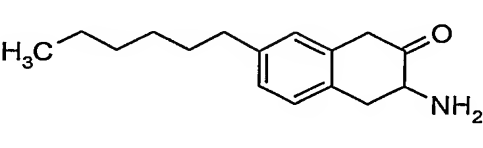
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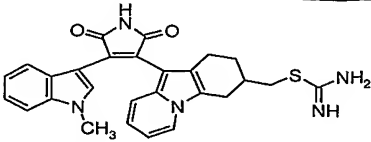
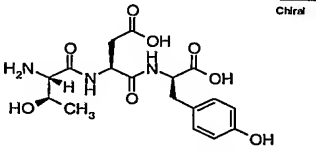
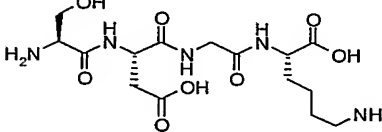
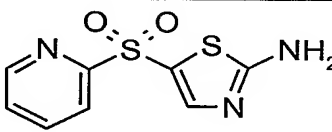
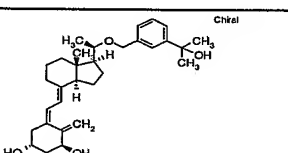
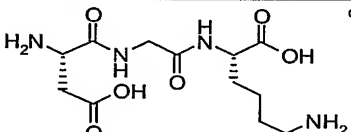
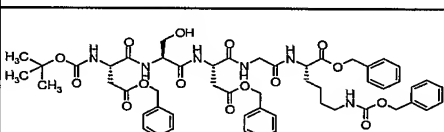
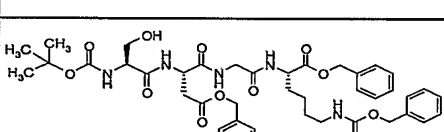
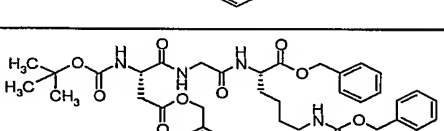
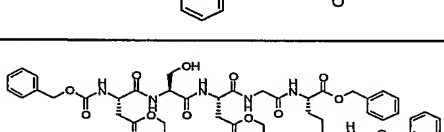
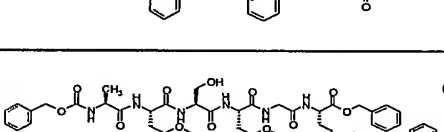
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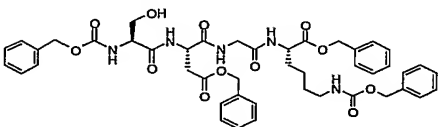
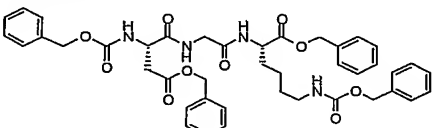
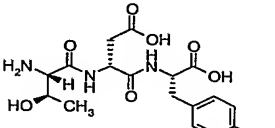
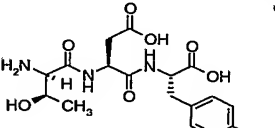
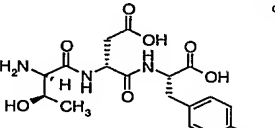
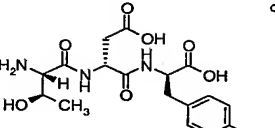
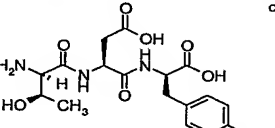
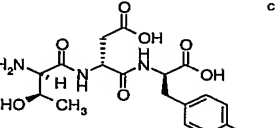
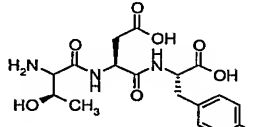
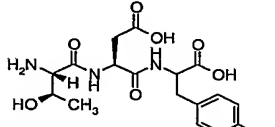
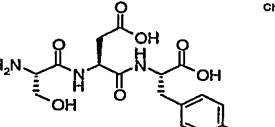
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| 1198 |  | Aventis Pharma | | EP 248734 |
| 1199 |  | Sumitomo Pharmaceuticals | | EP 248399 |
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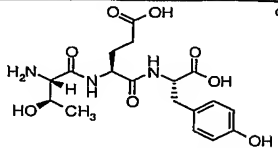
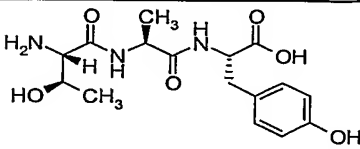
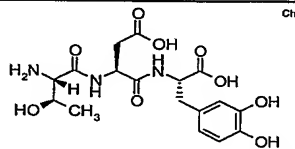
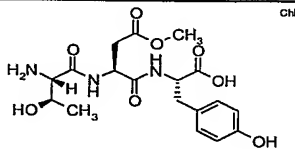
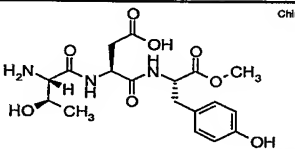
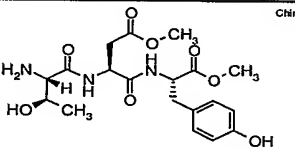
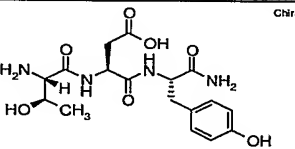
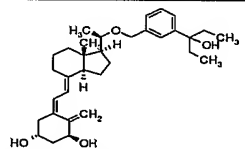
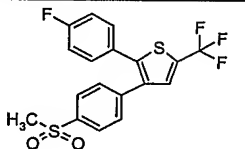
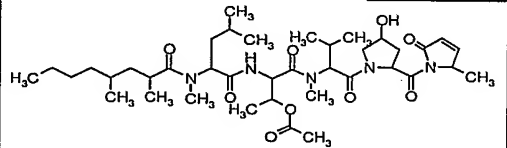
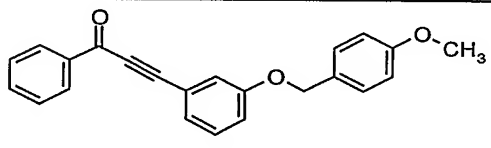
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| 1212 |  | Aventis Pharma | EP 248734 |
| 1213 |  | Pfizer | AU 8783281 |
| 1214 |  | Harbor Branch Found. | US 4755529 |
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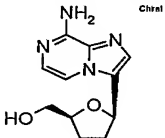
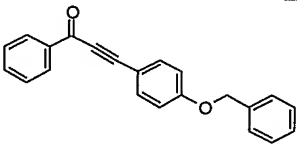
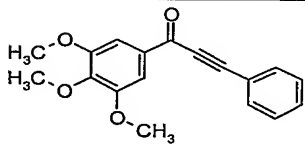
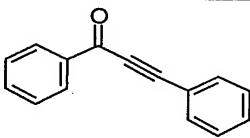
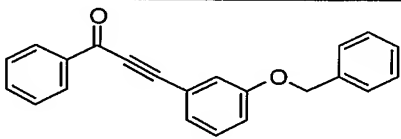
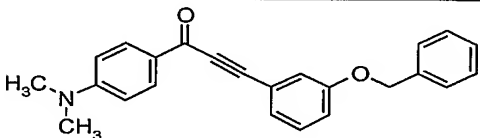
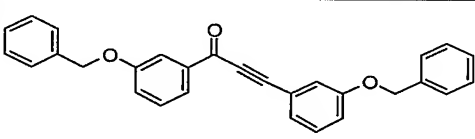
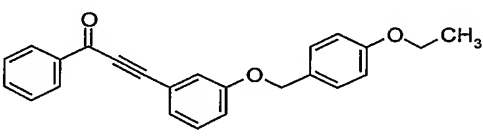
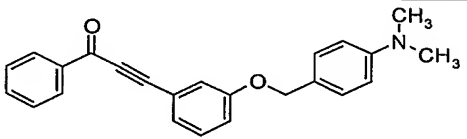
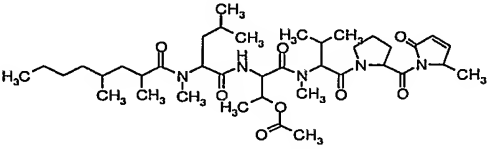
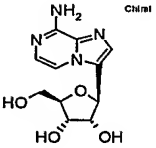
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| 1218 |  | Roche Bioscience | | AU 8782540 |
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| 1221 |  | Schering-Plough | | EP 318214 |
| 1222 |  Chiral | Novartis | | AU 8822785 |
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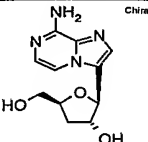
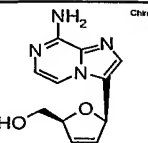
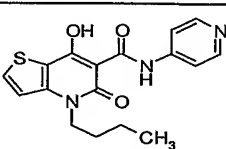
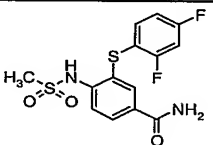
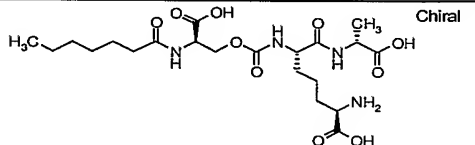
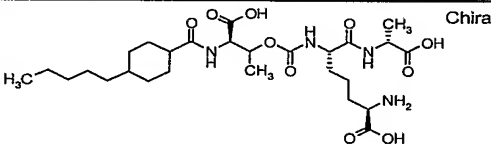
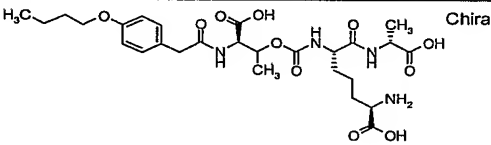
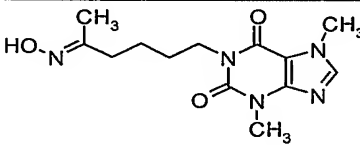
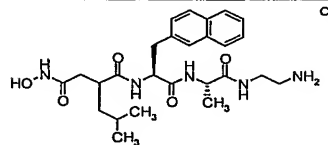
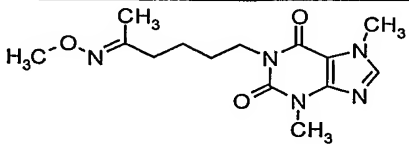
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| 1233 |  | Leo | | WO 8910351 |
| 1234 |  | Leo | | WO 8910351 |
| 1235 |  | Tanabe Seiyaku | 1) Ueno, M. et al. Jpn J Pharmacol 1992, 58(Suppl. 1): Abst O-210. | AU 8942368 |
| 1236 |  | Greenwich Pharm. | | AU 9047648 |
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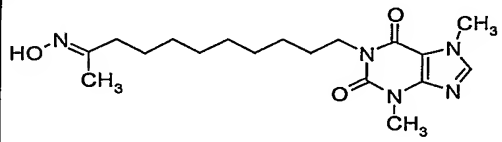
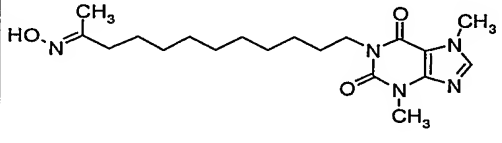
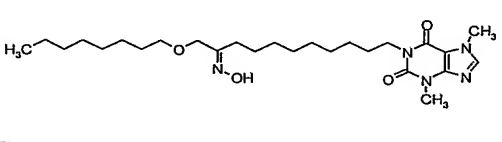
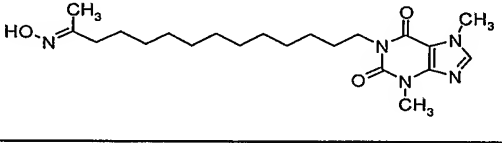
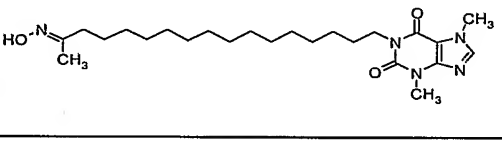
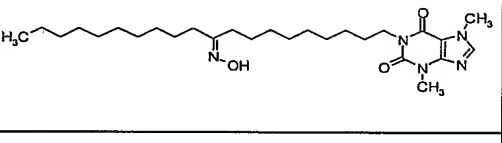
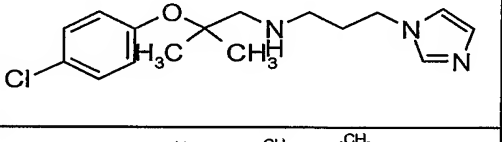
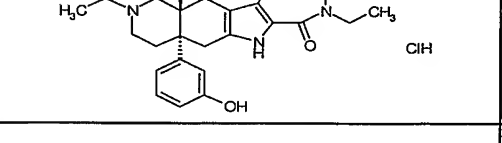
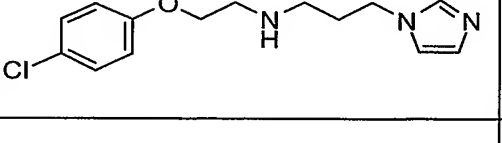
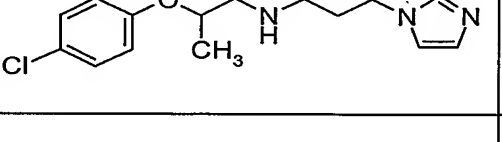
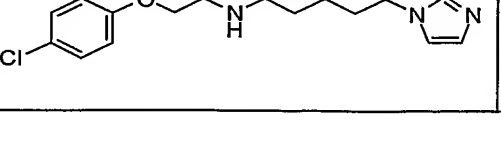
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| 1240 |  | Roche | | EP 384349 |
| 1241 |  | SPA | | EP 421074 |
| 1242 |  | Hitachi Chemical | | EP 421682 |
| 1243 |  | Fujisawa | 1) Manda, T. et al. Jpn J Pharmacol 1997, 73(Suppl. 1): Abst P-140. | EP 412404 |
| 1244 |  | Leo | | WO 9109841 |
| 1245 |  | Hitachi Chemical | | EP 421682 |
| 1246 |  | Hitachi Chemical | | EP 421682 |
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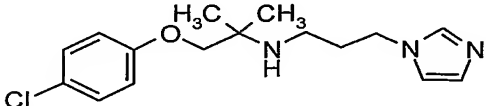
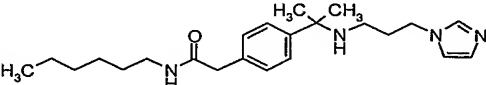
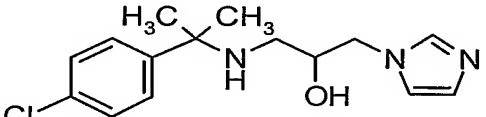
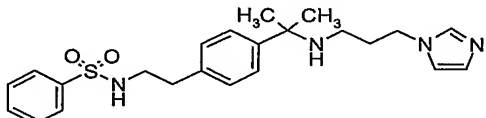
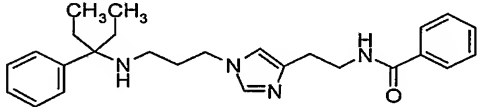
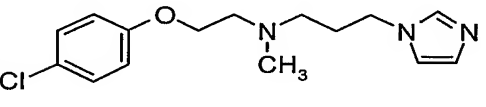
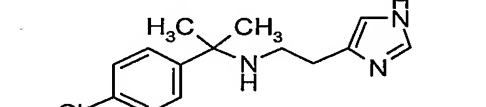
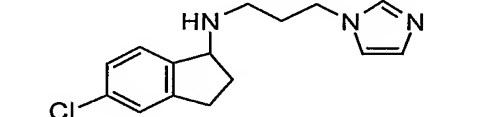
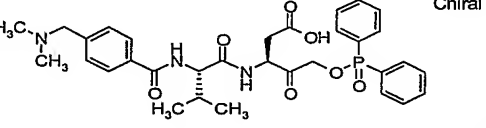
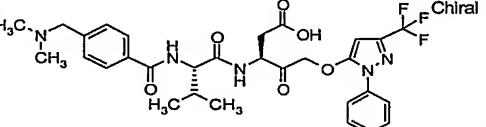
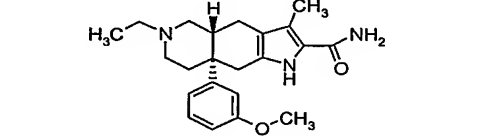
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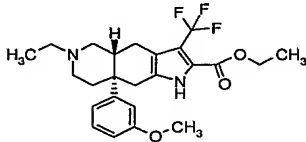
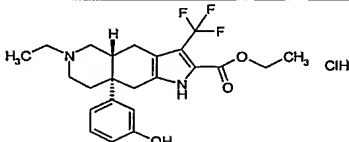
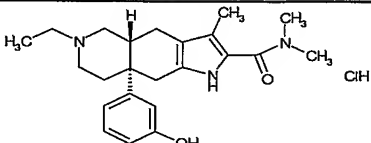
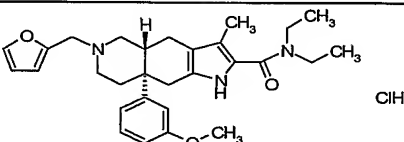
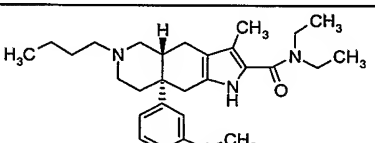
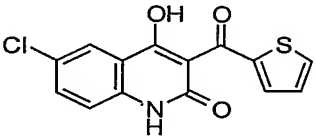
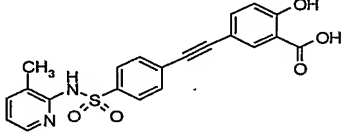
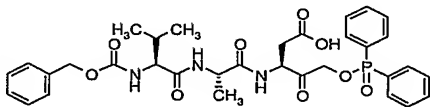
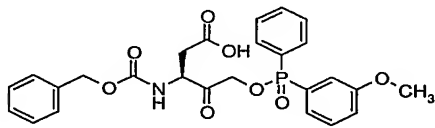
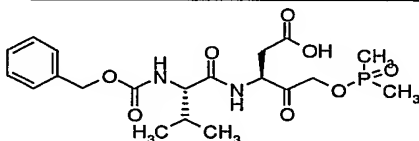
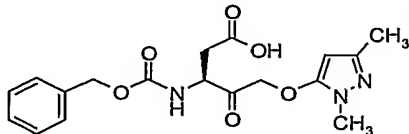
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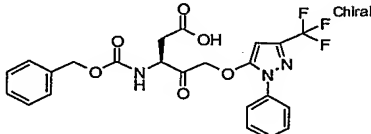
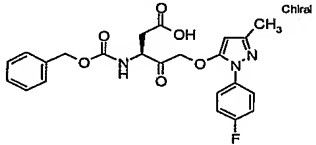
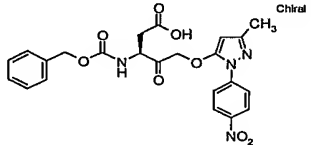
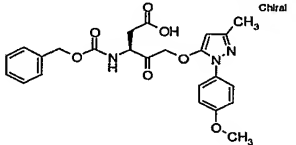
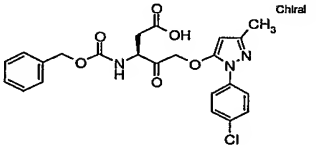
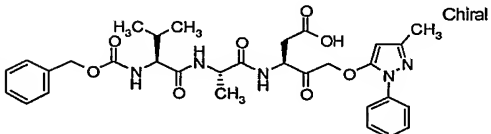
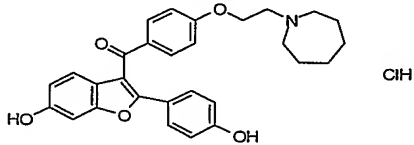
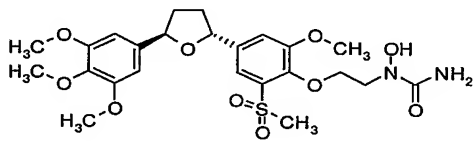
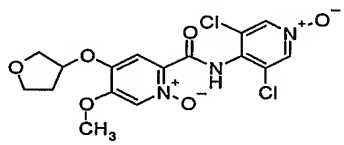
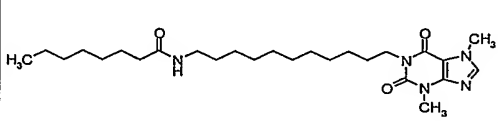
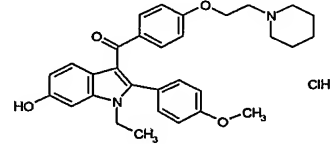
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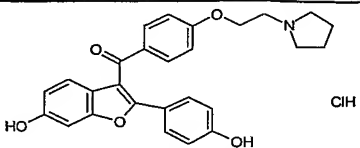
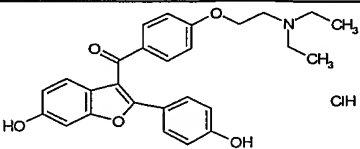
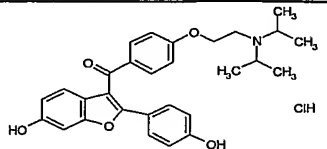
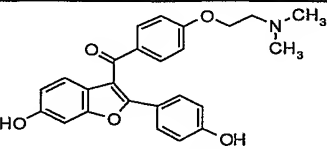
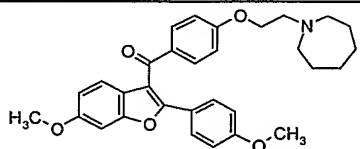
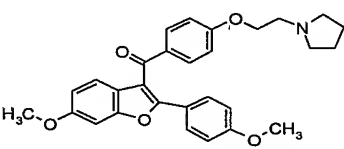
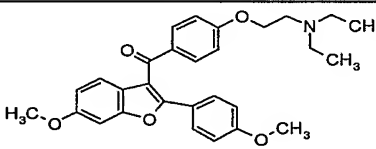
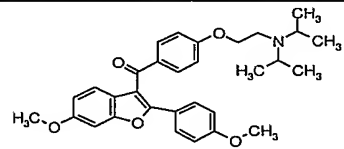
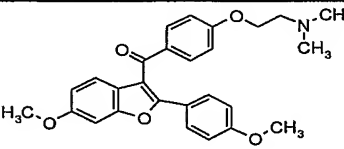
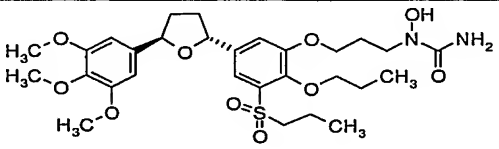
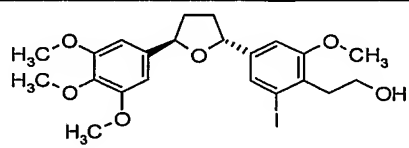
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| 1284 |  | Merck & Co. | | EP 480713 |
| 1285 |  | Merck & Co. | | EP 480713 |
| 1286 |  | Merck & Co. | | EP 480713 |
| 1287 |  | Kyowa Hakko | Miwa, K. et al. 113th Annu Meet Pharmaceut Soc Jpn (March 29-31, Osaka) 1993, Abst 30CC 13-1. | EP 505058 |
| 1288 |  | Fujisawa | Nakamura, K. et al. Chem Pharm Bull 1993, 41(5): 894. | AU 8783152 |
| 1289 |  | Wyeth | | US 5312831 |
| 1290 |  | Wyeth | | US 5312831 |
| 1291 |  | Wyeth | | US 5312831 |
| 1292 |  | Cell Therapeutics | | WO 9416704 |
| 1293 |  | Immunex | 1) Immunex Corporation Press Release 1994, July 21. | WO 9506031 |
| 1294 |  | Cell Therapeutics | | WO 9416704 |

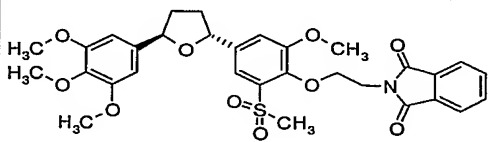
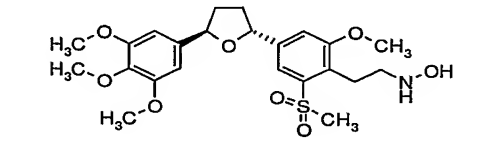
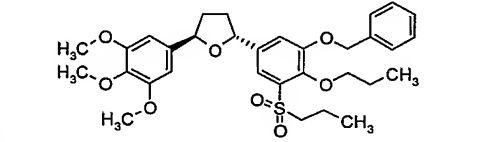
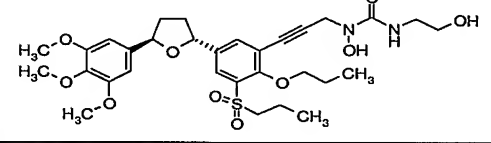
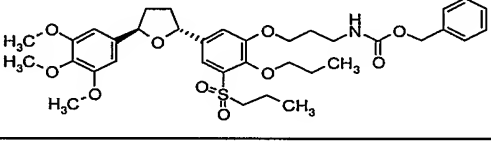
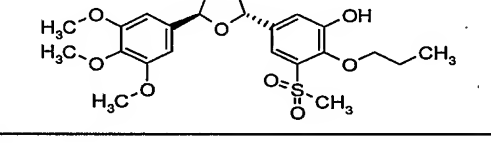
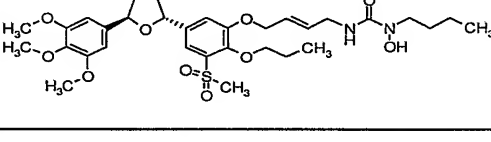
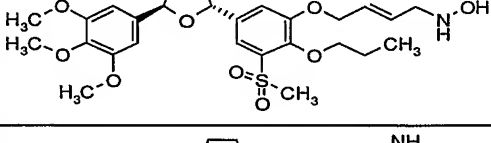
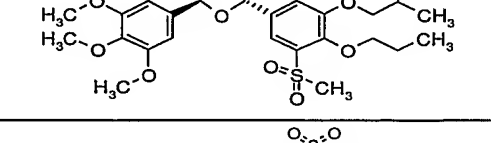
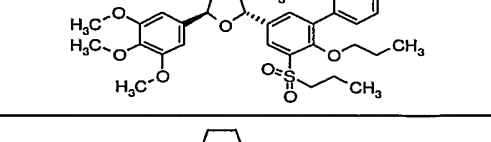
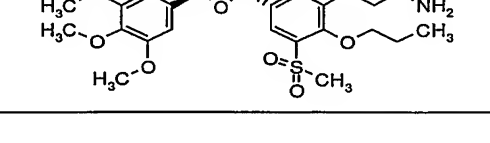
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| 1301 |  | Abbott GmbH | WO 9500493 |
| 1302 |  | GlaxoSmithKline | WO 9504734 |
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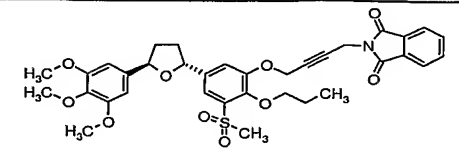
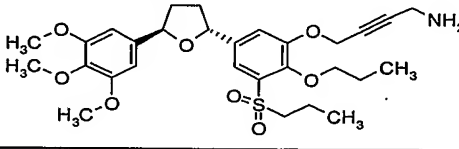
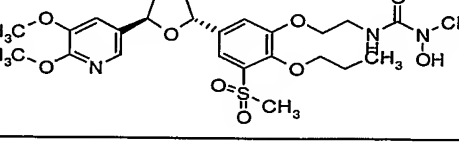
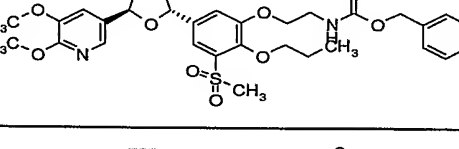
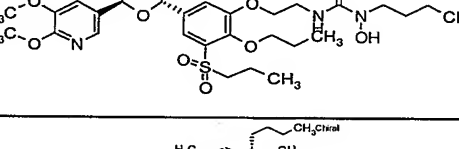
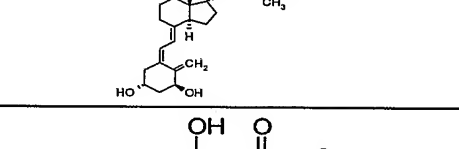
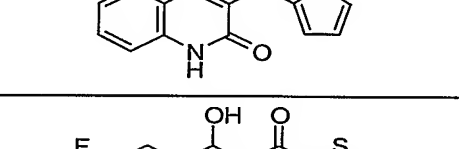
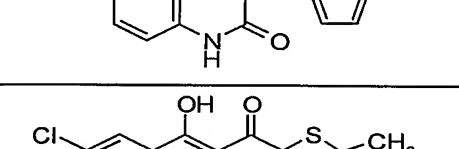
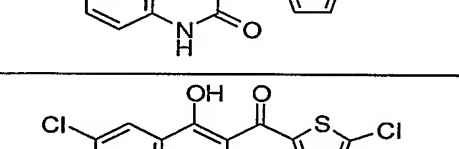
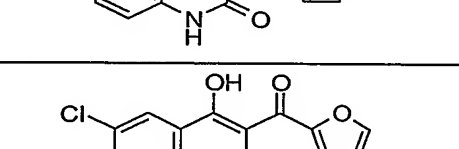
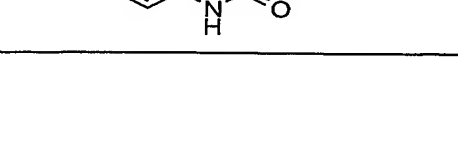
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| 1314 |  | Sanofi-Synthelabo | Chiral | EP 644197 |
| 1315 |  | Sanofi-Synthelabo | Chiral | CA 2125021 |
| 1316 |  | GlaxoSmithKline | | WO 9504734 |

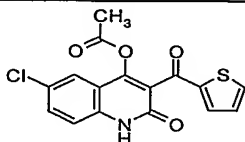
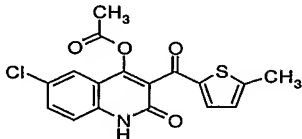
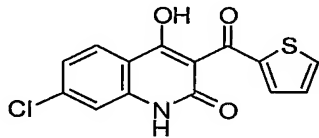
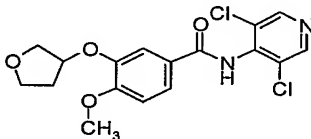
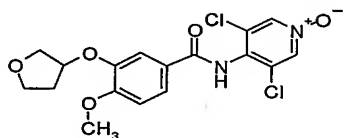
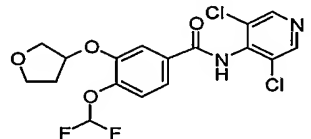
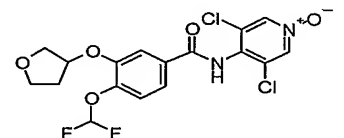
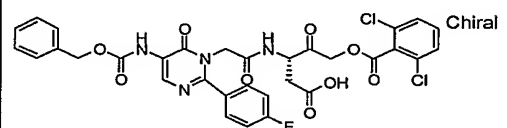
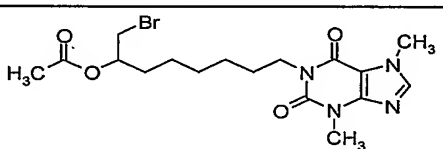
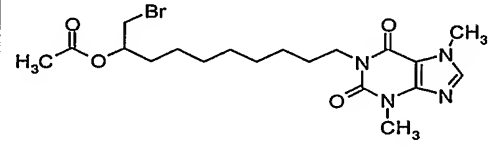
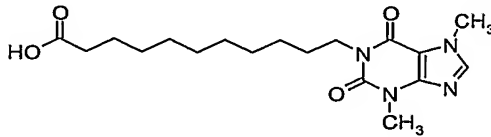
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| 1321 |  | GlaxoSmithKline | | WO 9504734 |
| 1322 |  | Japan Tobacco | | JP 95002779 |
| 1323 |  | Pharmacia | 1) Gozzi, P. et al. J Pharmacol Exp Ther 1999, 291(1): 199. | JP 1995501330 |
| 1324 |  Chiral | Sanofi-Synthelabo | | EP 644197 |
| 1325 |  Chiral | Sanofi-Synthelabo | | EP 644197 |
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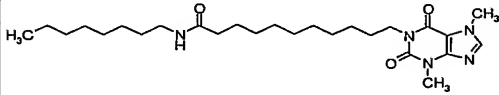
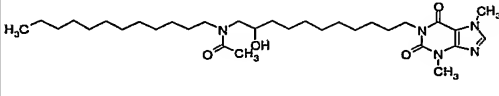
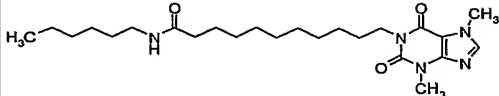
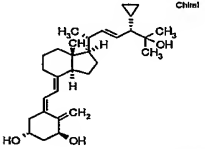
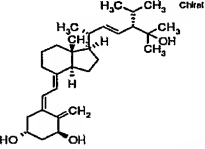
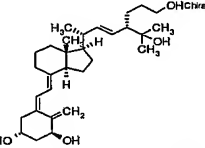
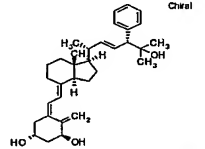
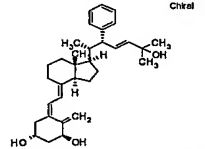
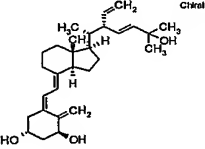
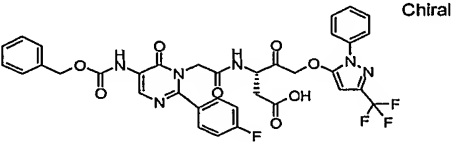
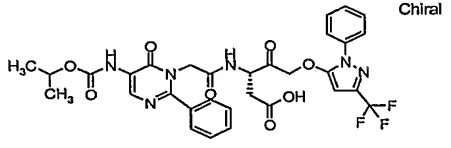
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| 1332 |  | Sanofi-Synthelabo | CA 2125021 |
| 1333 |  | Sanofi-Synthelabo | CA 2125021 |
| 1334 |  | Lilly | WO 9517382 |
| 1335 |  | Millennium | WO 9518610 |
| 1336 |  | Aventis Pharma | WO 9520578 |
| 1337 |  | Cell Therapeutics | WO 9522546 |
| 1338 |  | Lilly | WO 9517382 |

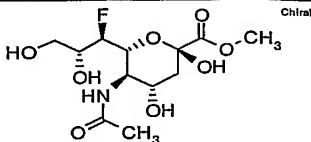
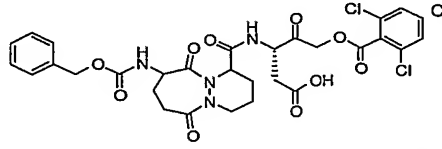
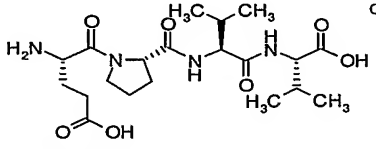
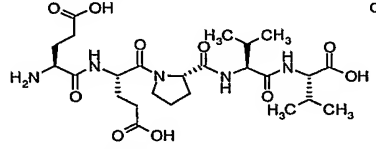
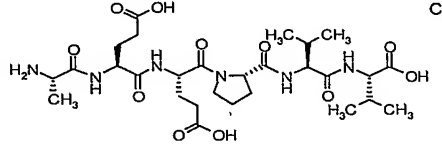
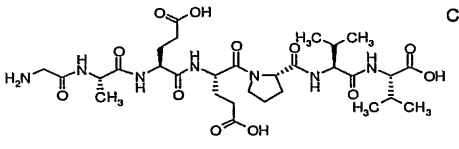
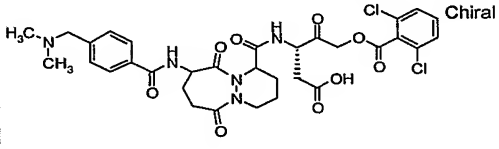
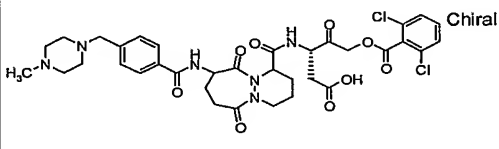
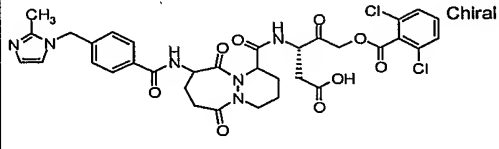
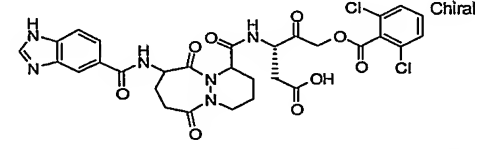
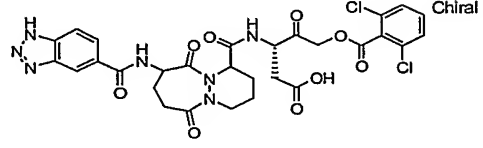
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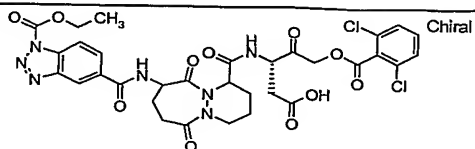
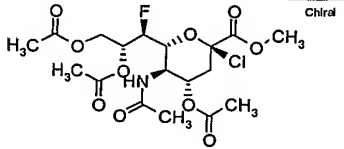
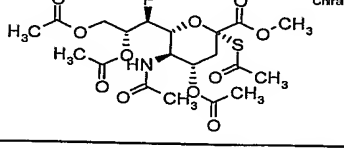
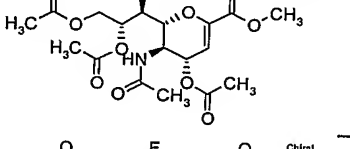
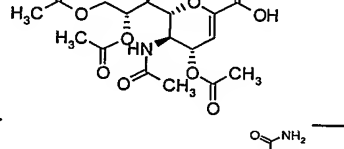
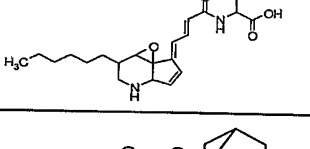
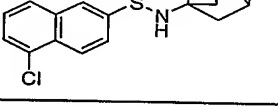
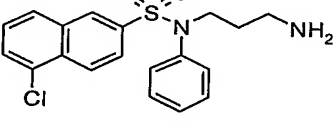
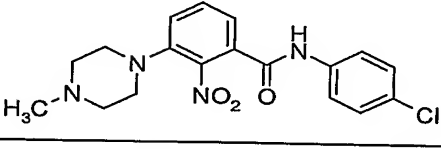
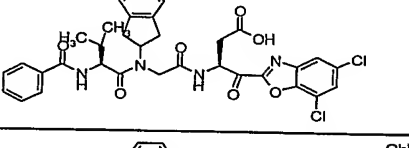
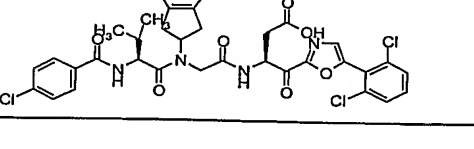
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| 1359 |  | CytoMed | WO 9518610 |
| 1360 |  | CytoMed | WO 9518610 |

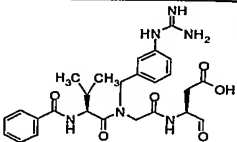
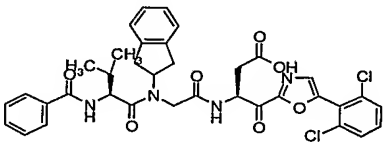
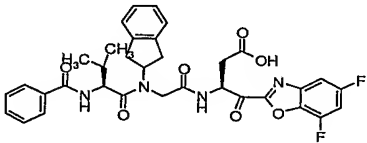
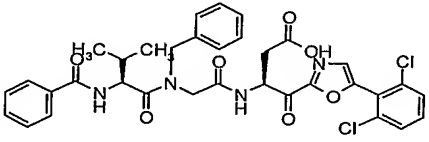
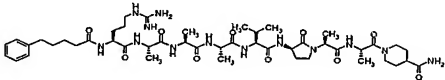
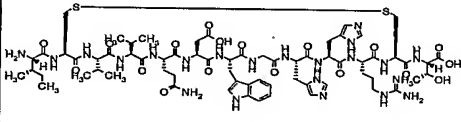
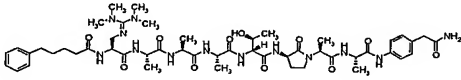
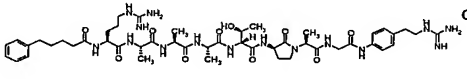
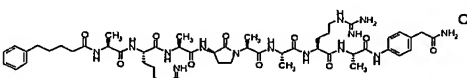
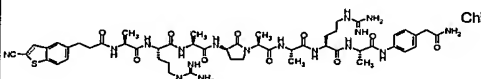
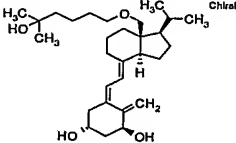
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| 1362 |  | CytoMed | WO 9518610 |
| 1363 |  | CytoMed | WO 9518610 |
| 1364 |  | CytoMed | WO 9518610 |
| 1365 |  | CytoMed | WO 9518610 |
| 1366 |  | Duphar | EP 664287 |
| 1367 |  | Japan Tobacco | JP 95002779 |
| 1368 |  | Japan Tobacco | JP 95002779 |
| 1369 |  | Japan Tobacco | JP 95002779 |
| 1370 |  | Japan Tobacco | JP 95002779 |
| 1371 |  | Japan Tobacco | JP 95002779 |

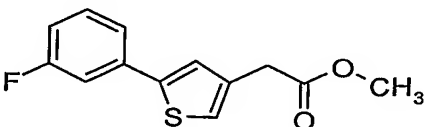
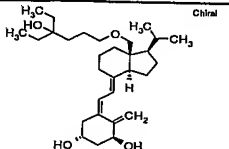
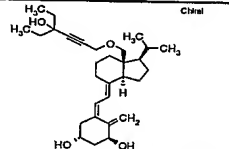
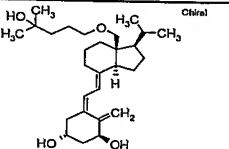
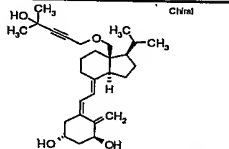
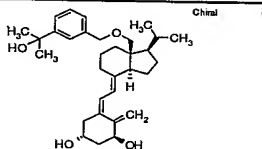
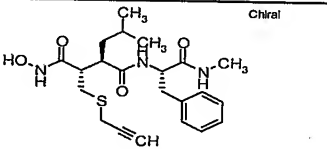
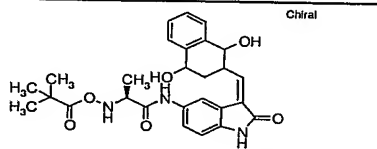
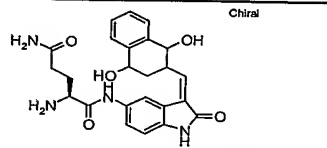
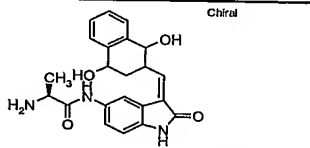
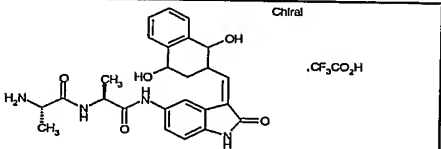
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| 1372 |  | Japan Tobacco | JP 95002779 |
| 1373 |  | Japan Tobacco | JP 95002779 |
| 1374 |  | Japan Tobacco | JP 95002779 |
| 1375 |  | Aventis Pharma | WO 9520578 |
| 1376 |  | Aventis Pharma | WO 9520578 |
| 1377 |  | Aventis Pharma | WO 9520578 |
| 1378 |  | Aventis Pharma | WO 9520578 |
| 1379 |  | Sanofi-Synthelabo | WO 9526958 |
| 1380 |  | Cell Therapeutics | WO 9522546 |
| 1381 |  | Cell Therapeutics | WO 9522546 |
| 1382 |  | Cell Therapeutics | WO 9522546 |

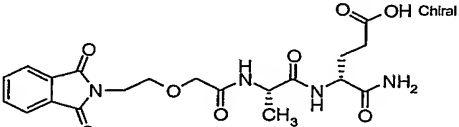
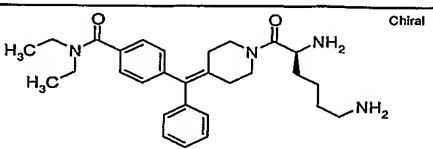
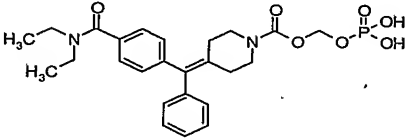
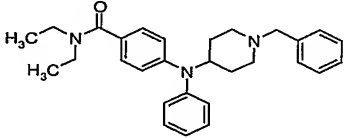
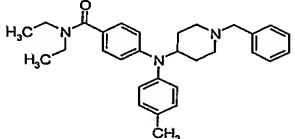
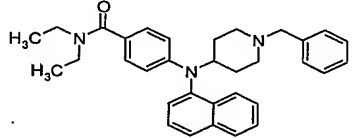
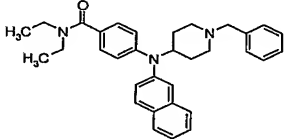
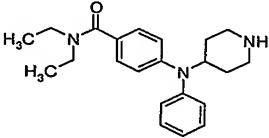
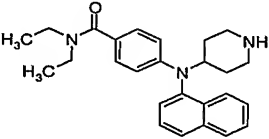
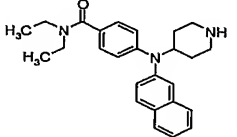
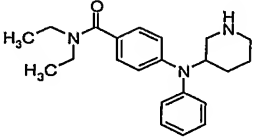
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| 1383 |  | Cell Therapeutics | WO 9522546 |
| 1384 |  | Cell Therapeutics | WO 9522546 |
| 1385 |  | Cell Therapeutics | WO 9522546 |
| 1386 |  | Duphar | EP 664287 |
| 1387 |  | Duphar | EP 664287 |
| 1388 |  | Duphar | EP 664287 |
| 1389 |  | Duphar | EP 664287 |
| 1390 |  | Duphar | EP 664287 |
| 1391 |  | Duphar | EP 664287 |
| 1392 |  | Sanofi-Synthelabo | WO 9526958 |
| 1393 |  | Sanofi-Synthelabo | WO 9526958 |

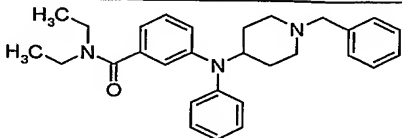
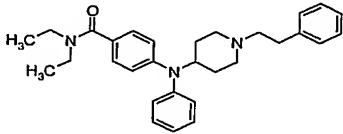
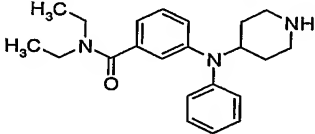
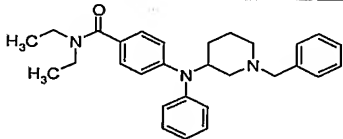
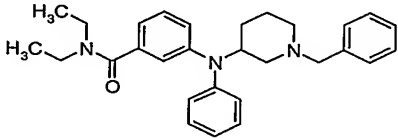
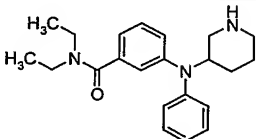
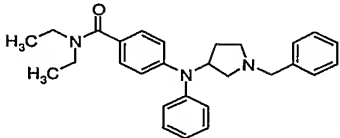
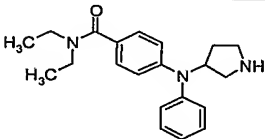
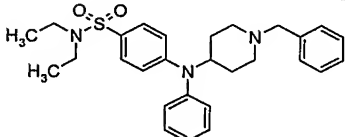
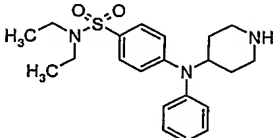
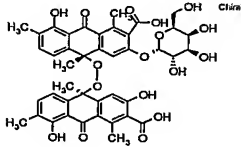
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| 1394 |  Chiral | Daikin | EP 711766 |
| 1395 |  Chiral | Sanofi-Synthelabo | WO 9533751 |
| 1396 |  Chiral | Ajinomoto | US 5464819 |
| 1397 |  Chiral | Ajinomoto | US 5464819 |
| 1398 |  Chiral | Ajinomoto | US 5464819 |
| 1399 |  Chiral | Ajinomoto | US 5464819 |
| 1400 |  Chiral | Sanofi-Synthelabo | WO 9533751 |
| 1401 |  Chiral | Sanofi-Synthelabo | WO 9533751 |
| 1402 |  Chiral | Sanofi-Synthelabo | WO 9533751 |
| 1403 |  Chiral | Sanofi-Synthelabo | WO 9533751 |
| 1404 |  Chiral | Sanofi-Synthelabo | WO 9533751 |

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| 1405 |  | Sanofi-Synthelabo | WO 9533751 |
| 1406 |  | Daikin | EP 711766 |
| 1407 |  | Daikin | EP 711766 |
| 1408 |  | Daikin | EP 711766 |
| 1409 |  | Daikin | EP 711766 |
| 1410 |  | Microbial Chemistry Research Foundation | JP 96176157 |
| 1411 |  | Tanabe | WO 9640641 |
| 1412 |  | Tanabe | WO 9640641 |
| 1413 |  | Daiichi Pharmaceutical | 1) Kawagoe, K. et al. AFMC Int Med Chem Symp (Sept 3-8, Tokyo) 1995, Abst P13M183. JP 97059236 |
| 1414 |  | Vertex | WO 9722618 |
| 1415 |  | Vertex | WO 9722618 |

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|------|---|----------------------------|--|------------|
| 1416 |  Chiral | Vertex | | WO 9722618 |
| 1417 |  Chiral | Vertex | | WO 9722618 |
| 1418 |  Chiral | Vertex | | WO 9722618 |
| 1419 |  Chiral | Vertex | | WO 9722618 |
| 1420 |  Chiral | AstraZeneca | | WO 9731023 |
| 1421 |  Chiral | University of Pennsylvania | | WO 9733603 |
| 1422 |  Chiral | AstraZeneca | | WO 9731023 |
| 1423 |  Chiral | AstraZeneca | | WO 9731023 |
| 1424 |  Chiral | AstraZeneca | | WO 9731023 |
| 1425 |  Chiral | AstraZeneca | | WO 9731023 |
| 1426 |  Chiral | Leo | | WO 9737972 |

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| 1427 |  | Taisho | | JP 97194476 |
| 1428 |  | Leo | | WO 9737972 |
| 1429 |  | Leo | | WO 9737972 |
| 1430 |  | Leo | | WO 9737972 |
| 1431 |  | Leo | | WO 9737972 |
| 1432 |  | Leo | | WO 9737972 |
| 1433 |  | GlaxoSmithKline | | WO 9743250 |
| 1434 |  | Pharmacia | | WO 9745409 |
| 1435 |  | Pharmacia | | WO 9745409 |
| 1436 |  | Pharmacia | | WO 9745409 |
| 1437 |  | Pharmacia | | WO 9745409 |

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| 1438 |  | LEK | | EP 477912 |
| 1439 |  | AstraZeneca | | WO 9828275 |
| 1440 |  | AstraZeneca | | WO 9828275 |
| 1441 |  | AstraZeneca | | WO 9828270 |
| 1442 |  | AstraZeneca | | WO 9828270 |
| 1443 |  | AstraZeneca | | WO 9828270 |
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| 1446 |  | AstraZeneca | | WO 9828270 |
| 1447 |  | AstraZeneca | | WO 9828270 |
| 1448 |  | AstraZeneca | | WO 9828270 |

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| 1449 |  | AstraZeneca | WO 9828270 |
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| 1451 |  | AstraZeneca | WO 9828270 |
| 1452 |  | AstraZeneca | WO 9828270 |
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| 1455 |  | AstraZeneca | WO 9828270 |
| 1456 |  | AstraZeneca | WO 9828270 |
| 1457 |  | AstraZeneca | WO 9828270 |
| 1458 |  | AstraZeneca | WO 9828270 |
| 1459 |  | Daiichi Pharmaceutical | Koiwa, T. et al. J Antibiot 1999, 52(2): 198. |

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| 1460 | Chiral | Bristol-Myers Squibb | WO 0244181 |
| 1461 | | Bristol-Myers Squibb | WO 0244181 |
| 1462 | | Bristol-Myers Squibb | WO 0244181 |
| 1463 | Chiral | Bristol-Myers Squibb | WO 0244181 |
| 1464 | Chiral | Bristol-Myers Squibb | WO 0244181 |
| 1465 | | Bristol-Myers Squibb | WO 0244181 |
| 1466 | | Bristol-Myers Squibb | WO 0244181 |
| 1467 | Chiral | Bristol-Myers Squibb | WO 0244181 |
| 1468 | | Bristol-Myers Squibb | WO 0244181 |
| 1469 | | Gruenenthal | WO 0290317 |

BRIEF DESCRIPTION OF SEQUENCE LISTING

| SEQ ID NO: | Description |
|------------|--|
| 1 | Draft genome assembly from The Genome Science Center in British Colombia, Canada of sequence from TOR2 isolate. <i>TOR2_draft_genome_assembly_120403 Release 1</i> |
| 2 | CDC SARS-CoV strain sequence. Entire nucleotide sequence (Urbani strain) |
| 3-20 | Group-specific coronavirus gene products > Feline infectious peritonitis virus (FIPV) 3/4 = ORF 3b; 5/6 = ORF 3X; 7/8 = ORF 3A > Canine coronavirus 9/10 = ORF 7b; 11/12 = ORF 7a > Avian infectious bronchitis virus 13/14 = ORF 5b; 15/16 = ORF 5a; 17/18 = ORF 3a; 19/20 = ORF 3b |
| 21-520 | 500 primers for left part |
| 521-1020 | 500 primers for right part |
| 1021-3520 | Forward primers from Table 4 |
| 3521-6020 | Reverse primers from Table 4 |
| 6021-6026 | Figure 9 primers |
| 6027-6033 | Figure 11 primers |
| 6034-6038 | Five primers from http://content.nejm.org/cgi/reprint/NEJMoa030781v2.pdf |
| 6039-6051 | PEP1 to PEP13 |
| 6052 | Extended PEP13 |
| 6053-6056 | 229E human coronavirus sequences |
| 6057-6060 | TGV sequences |
| 6061-6064 | PEDV sequences |
| 6065-6068 | Bovine coronavirus sequences |
| 6069-6071 | Murine hepatitis virus sequences |
| 6072-6075 | AIBV sequences |
| 6076-6170 | Primer sequences (forward) |
| 6171-6265 | Primer sequences (reverse) |
| 6266-6304 | Primer sequences (forward) |
| 6305-6343 | Primer sequences (reverse) |
| 6344-6366 | Primer sequences (forward) |
| 6367-6392 | Primer sequences (reverse) |
| 6393-6440 | Primer sequences (forward) F1-F48 |
| 6441-6487 | Primer sequences (reverse) R1-R47 |
| 6488-6559 | Primer sequences |
| 6560-6568 | Primer sequences |
| 6569 | The nsp2 proteinase (3CL-PRO) sequence in SARS coronavirus |
| 6570-72 | The nsp2 proteinases (3CLp) of avian IBV, MHV, and BCoV |
| 6573 | Consensus nsp2 proteinases sequence |
| 6574-6577 | IG sequences from Figure 18 |
| 6578 | Expression construct of nSh in pCMVIII |
| 6579 | Expression construct of nS in pCMVIII |
| 6580 | Expression construct of nSh ΔTC in pCMVIII |
| 6581 | Expression construct of nS ΔTC in pCMVIII |
| 6582 | Expression construct of nS1h in pCMVIII |
| 6583 | Expression construct of nS1 in pCMVIII |
| 6584-6585 | Primers for cDNA amplification |
| 6585-6587 | Primers for RT-PCR |
| 6588-6809 | Component sequences of Figure 23 (≥4 amino acids) |
| 6810-7179 | Component sequences of Figure 24 (≥4 amino acids) |
| 7180-7187 | N-glycosylation sites within SEQ ID NO: 6039 |
| 7188-7189 | Component sequences of Figure 25 |
| 7190 | Fragment of SEQ ID NO: 7188 |
| 7191 | Polynucleotide encoding SEQ ID NO: 7190 |
| 7192 | Amino acids 879-1005 of SEQ ID NO: 6042 |
| 7193 | Amino acids 879-980 of SEQ ID NO: 6042 |

| | |
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| 7194 | Amino acids 901-1005 of SEQ ID NO: 6042 |
| 7195 | Amino acids 1144-1201 of SEQ ID NO: 6042 |
| 7196 | Amino acids 1144-1196 of SEQ ID NO: 6042 |
| 7197-7199 | Membrane fusion peptide regions |
| 7200-7206 | NadA-based polypeptides |
| 7207-7223 | N-glycosylation sites within SEQ ID NO: 6042 |
| 7224-7231 | Slippage region |
| 7232 | Orf1ab polyprotein |
| 7233-7244 | Orf1ab polyproteins |
| 7245-7247 | X ₂ sequences for SEQ ID NOS 7233-7244 |
| 7248-7253 | Orf1ab polyproteins |
| 7254 | Zinc binding region 2 site |
| 7255-7271 | N-glycosylation sites in SEQ ID NOS: 6040-41,6043,6045-46,6050-51 |
| 7272-7291 | Polypeptides and polynucleotides |
| 7292-7293 | Intergenic sequences |
| 7294-7301 | Nucleotides from 5' end of SARSV genome followed by intergenic sequence |
| 7302-7306 | NadA constructs |
| 7307-7308 | Fragments of SEQ ID NO: 6042 |
| 7309 | NadA sequence |
| 7310-7311 | NadA leader sequences |
| 7312-7315 | Amino acid sequences from NadA |
| 7316-7324 | PCR primers |
| 7325-7330 | Primers |
| 7331 | CCACC sequence |
| 7332-7336 | 3' UTR forward primers |
| 7337-7341 | 3' UTR reverse primers |
| 7342-7352 | 3' UTR probes |
| 7353-7362 | 5' UTR forward primers |
| 7363-7373 | 5' UTR reverse primers |
| 7374-7385 | 5' UTR probes |
| 7386 | Conserved octanucleotide |
| 7387 | Reverse complement of SEQ ID NO: 7293 |
| 7388 | Intergenic sequence |
| 7389 | Poly T |
| 7390 | Stem-loop sequence |
| 7391-7392 | Poly-glycine linkers |
| 7393 | Poly-histidine tag |
| 7394 | Nucleocapsid epitope site |
| 7395 | Antisense primer |
| 7396-7397 | Probes |
| 7398-7399 | Antigenic fragments of SEQ ID NO: 6042 |
| 7400-7639 | T-epitope analysis of SEQ ID NO: 6039 |
| 7640-7800 | T-epitope analysis of SEQ ID NO: 6040 |
| 7801-8040 | T-epitope analysis of SEQ ID NO: 6041 |
| 8041-8280 | T-epitope analysis of SEQ ID NO: 6042 |
| 8281-8486 | T-epitope analysis of SEQ ID NO: 6043 |
| 8487-8665 | T-epitope analysis of SEQ ID NO: 6044 |
| 8666-8820 | T-epitope analysis of SEQ ID NO: 6045 |
| 8821-9018 | T-epitope analysis of SEQ ID NO: 6046 |
| 9019-9131 | T-epitope analysis of SEQ ID NO: 6047 |
| 9132-9308 | T-epitope analysis of SEQ ID NO: 6048 |
| 9309-9437 | T-epitope analysis of SEQ ID NO: 6049 |
| 9438-9538 | T-epitope analysis of SEQ ID NO: 6050 |
| 9539-9752 | T-epitope analysis of SEQ ID NO: 6052 |
| 9753-9763 | Primers for spike protein amplification, particularly fragments of spike |
| 9764-9765 | N-glycosylation sites within SEQ ID NO: 6039 |
| 9766-9779 | Cleavage products for ORF1ab (Table 10) |

| | |
|-----------|---|
| 9780-9782 | Forward primer, reverse primer, probe |
| 9783-9784 | Lysine-rich region |
| 9785-9798 | Oligonucleotides used for <i>S.cerevisiae</i> expression |
| 9799-9802 | Sequences from Figures 65 & 66 |
| 9803-9882 | Primers for <i>E.coli</i> cloning |
| 9883-9885 | BCV nucleotide sequences for Figures 3A, 3B, 3C |
| 9886-9891 | BCV amino acid sequences for Figures 4A, 4B, 4C, 4D, 4E, 4F |
| 9892 | BCV 5' UTR |
| 9893 | BCV 3' UTR |
| 9894-9896 | MHV nucleotide sequences for Figures 3A, 3B, 3C |
| 9897-9902 | MHV amino acid sequences for Figures 4A, 4B, 4C, 4D, 4E, 4F |
| 9903-9904 | AIBV nucleotide sequences for Figures 3A, 3B |
| 9905-9909 | AIBV amino acid sequences for Figures 4A, 4B, 4D, 4E, 4F |
| 9910 | AIBV 5' UTR |
| 9911 | AIBV 3' UTR |
| 9912-9913 | HOBMPRO, HOBHEGA nucleotide sequences for Figures 3B, 3C |
| 9914-9918 | Human CoV amino acid sequences for Figures 4A, 4B, 4C, 4E, 4F |
| 9919 | HCoV-OC43 5' UTR |
| 9920 | HCoV-OC43 3' UTR |
| 9921-9923 | pCMVKm2 vectors |
| 9924-9926 | Codon-optimised N, M and E sequences |
| 9927 | BNI-1 |
| 9928-9959 | Constituent amino acid sequences $\geq 4aa$ inferred from SEQ ID NO: 9927 |
| 9960 | ORF1ab variant |
| 9961 | ORF1a variant |
| 9962 | Spike variant |
| 9963 | Membrane variant |
| 9964 | Nucleocapsid variant |
| 9965-9966 | Short ORFs |
| 9967 | FRA complete genome |

CLAIMS

1. An isolated polypeptide of the SARS virus.
2. The polypeptide of claim 1, wherein the polypeptide is a Spike (S) polypeptide, an Env (E) polypeptide, a Membrane (M) polypeptide, a hemagglutinin-esterase polypeptide (HE), a
5 nucleocapsid (N) polypeptide, a ORF1a polypeptide, a ORF1ab polypeptide, a proteolytic fragment of a ORF1a polypeptide, or a proteolytic fragment of a ORF1ab polypeptide.
3. The polypeptide of claim 1, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6039, 7232, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 6042, 6043, 6044, 6045, 6046, 6047,
10 6048, 6049, 6050 or 6052.
4. The polypeptide of claim 1, wherein the polypeptide comprises an amino acid sequence having >75% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316,
15 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
5. The polypeptide of claim 1, wherein the polypeptide comprises a fragment of at least 10 consecutive amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769,
20 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
6. A polypeptide comprising an amino acid sequence having >80% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044,
25 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
7. A polypeptide comprising an amino acid sequence that comprises a fragment of at least
30 10 consecutive amino acids of an amino acid sequence selected from the group consisting SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.

8. A polypeptide comprising an amino acid sequence having >80% sequence identity to SEQ ID NO: 6042, and/or comprising an amino acid sequence that comprises a fragment of at least 10 consecutive amino acids of SEQ ID NO: 6042, wherein the polypeptide is in the form of a trimer.
- 5 9. Nucleic acid encoding the polypeptide of any one of claims 1 to 8.
10. Nucleic acid according to claim 9, comprising a nucleotide sequence selected from the group consisting of SEQ ID NO^S: 7191, 7273, 7275, 7277, 7279, 7281, 7283, 7285, 7287, 7289, 7291, 7292, 7293, 9968, 10066, 10084, 10299, 10505, 11323, 11563, 11639 & 11640.
- 10 11. A polynucleotide comprising a nucleotide sequence having >80% sequence identity to the nucleic acid of claim 9 or claim 10.
12. A polynucleotide comprising a fragment of at least 10 consecutive nucleotides of the nucleic acid of claim 9 or claim 10.
13. Antibody that recognizes the polypeptide of any one of claim 1 to 8.
14. The antibody of claim 13, wherein said antibody recognizes the polypeptide comprising
15 the amino acid sequence of SEQ ID NO: 6042 or a fragment thereof.
15. The antibody of claim 14, wherein said antibody recognizes the polypeptide comprising the amino acid sequence of SEQ ID NO: 6042 or a fragment thereof in trimeric form.
16. The antibody of claim 13, wherein the antibody is a monoclonal antibody,
17. The antibody of claim 13, wherein the antibody is a human antibody,
- 20 18. An immunoassay for detecting a SARS virus antigen in a sample, comprising the step of contacting the sample with the antibody of any one of claims 13 to 17.
19. An immunoassay for detecting an antibody against a SARS virus antigen in a sample, comprising the step of contacting the sample with the polypeptide of any one of claims 1 to 8.
20. A method of detecting an antibody against a SARS virus antigen in a sample comprising
25 contacting said sample with the polypeptide of any one of claims 1 to 8, under conditions suitable for binding said polypeptide to said antibody, if present, and detecting the binding of said polypeptide to said antibody.
21. A method for detecting a SARS virus antigen in a sample comprising contacting said
30 sample with the antibody of any one of claims 13 to 17, under conditions suitable for binding said antibody to said antigen, if present, and detecting the binding of said antibody to said antigen.

22. A vaccine for the treatment or prevention of severe acute respiratory syndrome (SARS), comprising an inactivated SARS virus, a killed SARS virus, an attenuated SARS virus, a split SARS virus preparation, or at least one purified SARS virus antigens.
23. The vaccine of claim 22, comprising a purified polypeptide according to any one of
5 claims 1 to 8.
24. The vaccine of claim 22 or claim 23, wherein the antigen is a purified SARS virus antigen in the form of a VLP.
25. The vaccine of any one of claims 22 to 24, further comprising an adjuvant.
26. The vaccine of claim 25, wherein the adjuvant is an aluminium salt or is MF59.
- 10 27. The vaccine of any one of claims 22 to 26, comprising more than one SARS virus antigen.
28. The vaccine of claim 27, wherein the antigens are selected from S, E, N and M.
29. The vaccine of claim 22, comprising an inactivated SARS virus.
30. The vaccine of claim 29, wherein said virus is inactivated by chemical or physical means.
- 15 31. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of detergents, formaldehyde, formalin, β -propiolactone, and UV light.
32. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of
20 methylene blue, psoralen and carboxyfullerene (C60).
33. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of binary ethylamine, acetyl ethyleneimine and gamma irradiation.
34. The vaccine of claim 31, wherein said inactivation comprises treatment with β -
25 propiolactone.
35. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.01 to 0.5%.
36. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.5 to 0.2%.
- 30 37. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.025 to 0.1%.

38. A method of inactivating SARS virus comprising exposing the virus to an inactivation agent for 12 to 24 hours at refrigeration temperatures followed hydrolysis of any residual inactivating agent by elevating the temperature for three hours.
39. The method of claim 38, wherein the inactivation agent is β -propiolactone.
- 5 40. The method of claim 38, wherein the refrigeration temperature is between 0°C and 8°C.
41. The method of claim 38, wherein the elevated temperature is between 33°C and 41°C.
42. A method for making an inactivated SARS vaccine comprising:
- a. innoculating a mammalian cell culture with SARS virus;
 - b. cultivating the infected cells;
 - 10 c. harvesting SARS virus containing supernatant;
 - d. inactivating the SARS virus; and
 - e. purifying the inactivated SARS virus.
43. The method of claim 42, wherein said mammalian cell culture is derived from one or more of the cell types selected from the group consisting of fibroblast cells, endothelial cells, 15 hepatocytes, keratinocytes, immune cells, mammary cells, smooth muscle cells, melanocyte cells, neural cells, prostate cells, renal cells, skeletal cells, liver cells, retinoblast cells and stromal cells.
44. The method of claim 42, wherein said mammalian cell culture is derived from a cell culture selected from the group consisting of human cells, non-human primate cells, HeLa cells, 20 human diploid cells, fetal rhesus lung cells, human embryonic kidney cells, VERO cells, horse cells, cow cells, sheep cells, dog cells, cat cells or rodent cells.
45. The method of claim 42, wherein said mammalian cell culture is derived from VERO cells or fetal rhesus kidney cells.
46. The method of claim 42, wherein said mammalian cells are cultured in serum free media.
- 25 47. The method of claim 42, wherein said mammalian cells are cultured in protein free media.
48. The method of claim 42, wherein said inoculating step comprising absorbing the SARS virus onto the cell culture for 60 to 300 minutes.
49. The method of claim 42, wherein said inoculating step is conducted at 25°C to 40°C.
- 30 50. The method of claim 42, wherein said purification step comprises one or more of the treatments selected from the group consisting of gradient centrifugation, ultracentrifugation, continuous-flow ultracentrifugation, chromatography, polyethylene glycol precipitation, and ammonium sulfate precipitation.

51. The method of claim 42, wherein said purification step comprises one or more of the treatments selected from the group consisting of ultrafiltration and dialfiltration.

52. The method of claim 50, wherein said chromatography treatment includes one or more of the chromatography treatments selected from the group consisting of ion exchange
5 chromatography, size exclusion chromatography, and liquid affinity chromatography.

53. The method of claim 52, wherein said chromatography treatment includes use of one more chromatographic resins selected from the group consisting of an anionic resin and a cationic resin.

54. The method of claim 52, wherein the ion exchange chromatography treatment includes a
10 first step using a strong anion exchange resin and a second step using a strong cation exchange resin.

55. The method of claim 50, wherein said gradient centrifugation purification step comprises density gradient centrifugation.

56. The method of claim 42, wherein said purification step comprises a first step of
15 chromatography purification and a second step of gradient centrifugation.

57. The method of claim 56, wherein said first chromatography purification step comprises liquid affinity chromatography.

58. The method of claim 56, wherein said second gradient centrifugation step comprises density gradient centrifugation.

59. A single-stranded oligonucleotide comprising a nucleotide sequence selected from the
20 group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

60. A single-stranded oligonucleotide comprising the complement of the oligonucleotide of claim 59.

61. The oligonucleotide of claim 59 or claim 60, comprising 10-30 nucleotides.
25

62. The oligonucleotide of claim 61, comprising the nucleotide sequence of SEQ ID NO: 7292, SEQ ID NO: 7293, the complement of SEQ ID NO: 7292 or the complement of SEQ ID NO: 7293.

63. A kit comprising primers for amplifying a template sequence contained within a SARS
30 virus nucleic acid target, the kit comprising a first primer and a second primer, wherein the first primer comprises a sequence substantially complementary to a portion of said template sequence and the second primer comprises a sequence substantially complementary to a portion of the

complement of said template sequence, wherein the sequences within said primers which have substantial complementarity define the termini of the template sequence to be amplified.

64. The kit of claim 63, wherein the template sequence is contained within SEQ ID NO: 1 and/or SEQ ID NO: 2.

5 65. The kit of claim 63 or claim 64, wherein the first primer comprises a fragment of 8 or more nucleotides of SEQ ID NO: 1, and the second primer comprises a fragment of 8 or more nucleotides of the complement of SEQ ID NO: 1.

66. The kit of claim 63 or claim 64, wherein the first primer comprises a fragment of 8 or more nucleotides of SEQ ID NO: 2, and the second primer comprises a fragment of 8 or more
10 nucleotides of the complement of SEQ ID NO: 2.

67. The kit of claim 63, wherein the first primer is an oligonucleotide according to any one of claims 59 to 62 and the second primer is an oligonucleotide according to any of claims 59 to 62.

68. The kit of any one of claims 63 to 67, further comprising a labeled probe that comprises either a fragment of 8 or more nucleotides of SEQ ID NO: 1 and/or SEQ ID NO: 2, or the
15 complement of said fragment, which fragment is located within the template sequence.

69. The kit of any one of claims 63 to 68, wherein the first primer and/or the second primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

70. The kit of any one of claims 63 to 68, wherein the first primer and/or the second primer comprises the complement of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

71. A method of detecting the presence of SARS virus in a sample comprising providing a
5 sample suspected of containing a SARS virus nucleic acid target, amplifying a template sequence contained within said SARS virus nucleic acid target with the kit of any one of claims 63 to 70, and detecting the amplified template sequence, wherein the presence of the amplified template sequence indicates the presence of SARS virus in said sample.

72. The method of claim 71, wherein said amplifying is accomplished using polymerase
0 chain reaction, transcription mediated amplification, reverse transcription PCR, ligase chain reaction, strand displacement amplification or nucleic acid sequence-based amplification.

73. A double-stranded RNA molecule with a length from about 10 to about 30 nucleotides which is able to inactivate the SARS coronavirus in a mammalian cell.

74. The double-stranded RNA of claim 73, wherein the sequence of one of the strands is at least 90% identical to a target sequence, wherein the target sequence is a fragment of SEQ ID NO: 1 and/or SEQ ID NO: 2.
75. The double-stranded RNA of claim 73 or claim 74, wherein the target sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 7292, 7293, 7294, 7295, 7296, 7297, 7298, 7299, 7300 and 7301.
76. The double-stranded RNA of any one of claims 73 to 75, comprising at least one modified nucleotide.
77. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a molecule of less than 1000 g/mol.
78. The method of claim 77, wherein the molecule has an aromatic region and greater than one heteroatom selected from O, S, or N.
79. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a compound selected from: a nucleoside analog, a peptoid, an oligopeptide, a polypeptide a protease inhibitor, a 3C-like protease inhibitor, a papain-like protease inhibitor, or an inhibitor of an RNA dependent RNA polymerase.
80. A method for treating a patient suffering from SARS, comprising: administering to the patient a steroidal anti-inflammatory drug in combination with at least one antiviral compound.
81. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a compound selected from: acyclovir, gancyclovir, vidarabidine, foscarnet, cidofovir, amantidine, ribavirin, trifluorothymidine, zidovudine, didanosine, zalcitabine, an antiviral compound listed in Table 1; an antiviral compound listed in Table 2; or an interferon.
82. The method of claim 81, wherein the interferon is an interferon- α or an interferon- β .
83. The method of any one of claims 77 to 82, wherein the molecule or compound is delivered by inhalation.
84. A method of identifying a therapeutically active agent comprising the steps of: (a) contacting a therapeutically active agent with a cell infected with the SARS virus; (b) measuring attenuation of a SARS related enzyme.
85. A viral vector or particle for *in vivo* delivery of a nucleic acid of claim 9 or claim 10.
86. The viral vector of claim 85, wherein the vector is an adenovirus vector, a poxvirus vector or an alphavirus vector.
87. An alphavirus replicon particle comprising one or more SARS viral antigens.

88. The replicon particle of claim 87, wherein said SARS viral antigen is a spike protein.
89. The replicon particle of claim 87, wherein said particle comprises a replicon derived from Venezuelan Equine Encephalitis (VEE) and further comprises an envelope derived from Sindbus virus (SIN) or Semliki Forest Virus (SFV).
- 5 90. A vaccine comprising one or more SARS virus antigens and one or more respiratory virus antigens.
91. The vaccine of claim 90, wherein said respiratory virus antigens are selected from the group consisting of influenza virus, human rhinovirus (HRV), parainfluenza virus (PIV), respiratory syncytial virus (RSV), adenovirus, metapneumovirus, and rhinovirus.
- 10 92. The vaccine of claim 91, wherein said respiratory virus antigen is from influenza virus.
93. The vaccine of claim 90, wherein said respiratory virus antigen is from a coronavirus other than the SARS virus.
94. A polypeptide comprising an immunogenic, surface exposed fragment of the amino acid sequence SEQ ID NO: 6042.
- 15 95. The polypeptide of claim 94, wherein said fragment does not include the last 50 amino acids of the C-terminus of SEQ ID NO: 6042.
96. The polypeptide of claim 94, wherein said fragment does not include a transdomain region of SEQ ID NO: 6042.
97. The polypeptide of claim 94, wherein said fragment does not include a C-terminus
20 cytoplasmic domain of SEQ ID NO: 6042.
98. The polypeptide of claim 94, wherein said fragment does not include a N-terminus signal sequence.
99. An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066.
- 25 100. The polynucleotide of claim 99, wherein the polynucleotide comprising a nucleic acid sequence having > 80% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066.
101. An isolated polynucleotide comprising a fragment of at least 15 consecutive nucleic acids of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066
30 and wherein said fragment does not consist entirely of SEQ ID NO: 10033.
102. An isolated polypeptide comprising an amino acid sequence encoded by any one of claims 99 – 101.

103. The polypeptide of claim 102, comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 9969 – 10032, 10067, and 10015.
104. The polypeptide of claim 103, wherein the amino acid sequence is selected from the group consisting of SEQ ID NOS: 9997, 9998 and 10015.
- 5 105. An expression construct for recombinant expression of a SARS virus spike protein wherein said construct comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 6578 – 6583.
106. A mammalian cell line stably expressing a SARS viral antigen.
107. The cell line of claim 106, wherein said cell line is a Chinese Hamster Ovary (CHO) cell.
- 10 108. The cell line of claim 106, wherein the SARS viral antigen is a spike protein or fragment thereof.
109. The cell line of claim 106, wherein the spike protein is truncated to remove the transmembrane sequence.
110. A method of identifying a therapeutically active agent comprising the steps of: (a)
- 15 contacting a therapeutically active agent with a buffer comprising SARS enzyme; and (b) measuring attenuation of the SARS enzyme.
111. The method of claim 110 wherein the SARS enzyme is a SARS protease.
112. The method of claim 111 wherein the buffer further comprises a peptide with a SARS protease cleave site.
- 20 113. The method of claim 110 wherein the measurement is made by the measurement of fluorescence.
114. A vaccine of one of claims 22 to 37, and 90 to 93 further comprising an adjuvant.
115. The vaccine of claim 114 wherein the adjuvant is a SMIP.
116. The vaccine of claim 115 wherein the SMIP compound is selected from the group
- 25 consisting of an acylpiperazine, a tryptanthrin, an indoleione, a tetrahydroisoquinoline, a benzocyclodione, an amino azavinyl compound, a thiosemicarbazone, a lactam, an aminobenzimidazole quinolinone, a hydrophthalamide, a benzophenone, an isoxazole, a sterol, a quinazolinone, a pyrole, an anthraquinone, a quinoxaline, a triazine, an benzazole, and a pyrazolopyrimidine, or a pharmaceutically acceptable salt, ester, or prodrug thereof.
- 30 117. A method of vaccinating a subject comprising administering a vaccine of one of claims 22 to 37, and 90 to 93.
118. The method of claim 117 further comprising administering a SMIP.

119. A method for treating a patient of one of claims 77 to 82 further comprising administering at least one SMIP compound.

120. A method for treating a patient of one of claims 77 to 82 further comprising administering at least one SMIS compound.

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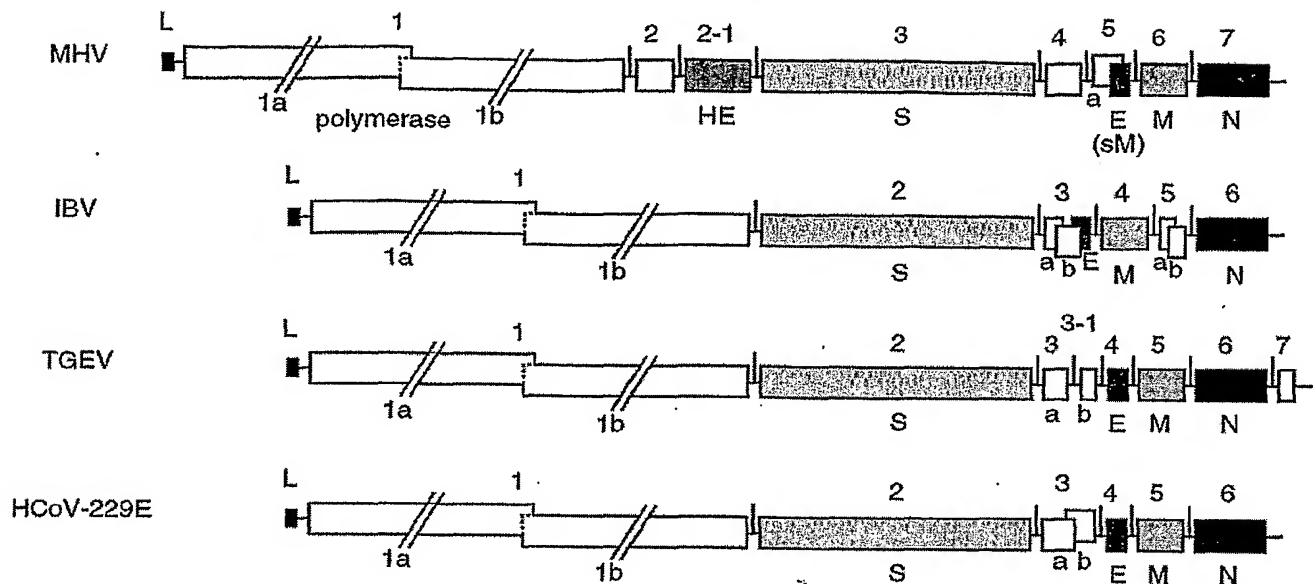
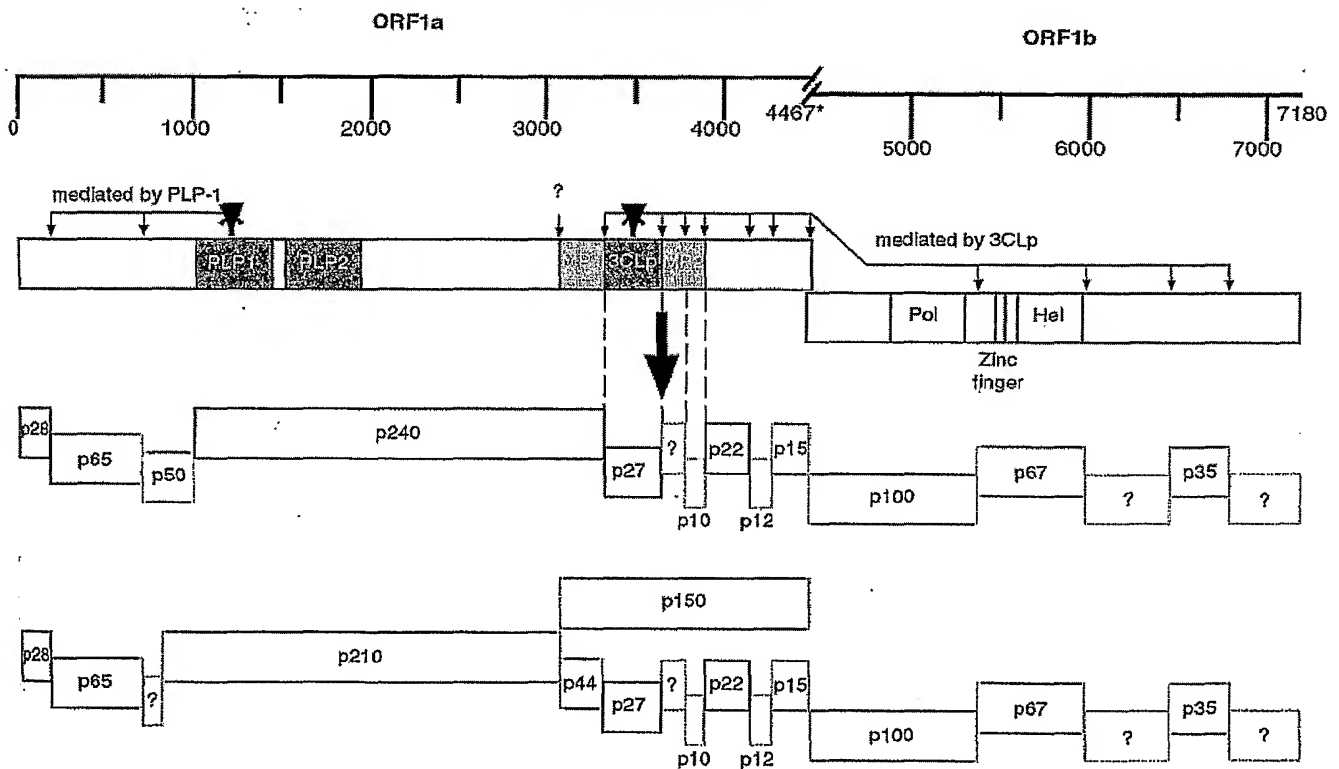
FIGURE 1**FIGURE 2**

FIGURE 3**FIGURE 3A**

| | | Section 1 | | | | |
|-------------------------------|-------|---------------------|------------------------|----------------------|------------------|-------|
| | | (1) 1 | 10 | 20 | 30 | 43 |
| BCV N | (1) | ATGTCTTTT | ACTCCTGGT | -AAGCAAT- | -CCAGTAGTAGAGCGT | |
| MHV N | (1) | ATGTCTTTT | GTTCTGGGG | CAAGAAAATG | CCGGTGGCAGAAAGCT | |
| Avian infectious bronchitis N | (1) | ----- | ----- | ----- | ----- | ----- |
| Consensus | (1) | ATGTCTTTT | TCCTGG | AAG AA | CC GT G AGA | T |
| | | Section 2 | | | | |
| | | (44) 44 | 50 | 60 | 70 | 86 |
| BCV N | (41) | CGTTTGGAAT | CGTTCTGGTAAT | GCCATCCTTAAG | ----- | ----- |
| MHV N | (44) | CCTCTGTAAACCG | CGCTGGTAATGGAAT | CCTCAAGAAGACCAC | | |
| Avian infectious bronchitis N | (1) | ----- | ----- | ----- | ----- | ----- |
| Consensus | (44) | CCT TG AAA CG | CTGGTAATGG | ATCCT AAG | | |
| | | Section 3 | | | | |
| | | (87) 87 | 100 | 110 | | 129 |
| BCV N | (76) | -TGGGCGGATCAGT | CCGACCAATCTAGAAA | TGTTCAAACCAGG | | |
| MHV N | (87) | TTGGGGCTGACCAAAC | CGAGCGTGGACCAAA | TAATCAAAATAGA | | |
| Avian infectious bronchitis N | (1) | ----- | -ATGGCGAGCGGTAAAG | CAGCTGGAAAGTCAGA | | |
| Consensus | (87) | TGGGC GA CA | CCGAGCG T AAGAAAT | TCAA CAGA | | |
| | | Section 4 | | | | |
| | | (130) 130 | 140 | 150 | 160 | 172 |
| BCV N | (118) | GGTAGAAGAGCTCA | ACCCAAAGGAAACT | GGTACTTCTCAGCTAC | | |
| MHV N | (130) | GGCAGAAGGAATCAG | CCAAGCAGACTGCAACT | ACTCAAC--C | | |
| Avian infectious bronchitis N | (33) | CTGCCCCGCGCCAATC | ---ATCAAAC | TAGGAGGACCAAAA--C | | |
| Consensus | (130) | GGCAGAAG GCTCA | CC AAGCAAAC | TGC ACTACTCAAC | C | |
| | | Section 5 | | | | |
| | | (173) 173 | 180 | 190 | 200 | 215 |
| BCV N | (161) | CATCAGGAGGGAATG | TGTGTACCCCTACTAT | -TCTTGCTTCTCTG | | |
| MHV N | (171) | CAACTCC-GGGAGTGT | GGTTCCCCATTAC | -TCCTGGTTTCTGTG | | |
| Avian infectious bronchitis N | (71) | CACCAAA-GGTAGGGT | CATCTGGAAATGCATCT | TGGTTTCAAG | | |
| Consensus | (173) | CA CA | GGGAGTGT GT CCC A | TAC TCTTGTTTTTCTG | | |
| | | Section 6 | | | | |
| | | (216) 216 | 230 | 240 | | 258 |
| BCV N | (203) | GAATTAA--CTCAGTTT | CAAAAAGGAAAGGAGTTT | GAATTTGC | | |
| MHV N | (212) | GCATTAA--CCCAGTTT | CAAAAAGGAAAGGAGTTT | CAGTTTGC | | |
| Avian infectious bronchitis N | (113) | CCATAAAGGCCAAAGAACT | AAATGCACCTGCACCTAAGTTG | | | |
| Consensus | (216) | GCATTAA | CCCAGTT CAAAA | GGAAAGGAGTTT AGTTTGC | | |
| | | Section 7 | | | | |
| | | (259) 259 | 270 | 280 | 290 | 301 |
| BCV N | (243) | AGAGGGACAAGGTGTG | CCTATTGCAACAGGAGT | CCCAGCTACT | | |
| MHV N | (252) | AGAAGGACAAGGAGT | GCCTATTGCCAATGGAAT | CCCCGCTTCA | | |
| Avian infectious bronchitis N | (155) | --AAGGTAGTGCTGT | TCTGATAATGAAAATCT | TAAAAATAGC | | |
| Consensus | (259) | AGAAGGACAAGGTGTG | CCTATTGC | AAGGA TCCCAGCTAC | | |

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FIGURE 3A (contd.)

| | | | | | | Section 8 |
|-------------------------------|-------|--|-----|-----|-----|------------|
| | (302) | 302 | 310 | 320 | 330 | 344 |
| BCV N | (286) | GAAGCTAAGGGGTACTGGTACAGACACAACAGACGTTCTTTTA | | | | |
| MHV N | (295) | GAGGAAAAGGGATATTGGTATAGACACAACCGCCGTTCTTTTA | | | | |
| Avian infectious bronchitis N | (196) | CAGCAGCACGGTACTGGAGGCGCCAAAGCCAG-----GTTTA | | | | |
| Consensus | (302) | GAGCA AAGGGGTACTGGTA AGACACAACAG CGTTCTTTTA | | | | |
| | | | | | | Section 9 |
| | (345) | 345 | 350 | 360 | 370 | 387 |
| BCV N | (329) | AAACAGCCGATGGCA-ACCAGCGTCAACTGCTGCCACCGATGGT | | | | |
| MHV N | (338) | AAACACCTGATGGGC-AGCAGAGCAATTACTGCCCAGATGGT | | | | |
| Avian infectious bronchitis N | (233) | AGCCAGGTAAAGGCGGAGAAAACCAAGTCCCTGATGCC-TGGT | | | | |
| Consensus | (345) | AAACAGCTGATGGC A CAGAA CAATT CTGCC CGATGGT | | | | |
| | | | | | | Section 10 |
| | (388) | 388 | 400 | 410 | 420 | 430 |
| BCV N | (371) | ATTTTACTATCTTGGAAACAGGACCGCATGCCAAGACCAGTA | | | | |
| MHV N | (380) | ATTTTACTATCTTGGCACAGGGGCCCATGCTGGAGCCAGTTA | | | | |
| Avian infectious bronchitis N | (275) | ATTTCTATTACACTGGAAGAGGACCAGCCGCTGACCTGAATTG | | | | |
| Consensus | (388) | ATTTTACTATCTTGGAAACAGGACC CATGCTGAAG CAATTA | | | | |
| | | | | | | Section 11 |
| | (431) | 431 | 440 | 450 | 460 | 473 |
| BCV N | (414) | TGGCACCGATATTGACGGAGTCTTCTGGGTGCTAGTAACCCAG | | | | |
| MHV N | (423) | TGGAGACAGCATTGAAGGTGTCTTCTGGGTGCAAAACAGCCAA | | | | |
| Avian infectious bronchitis N | (318) | GGGTGATTCTCAAGATGGTATAGTGTGGGTGGCTGCTAAGGGT | | | | |
| Consensus | (431) | TGG GAC TATTGA GGTGTCTTCTGGGTTGCTA TAACCA | | | | |
| | | | | | | Section 12 |
| | (474) | 474 | 480 | 490 | 500 | 516 |
| BCV N | (457) | GCTGATGTCAATACCCCGGCTGACATTCTCGATCCGGAGCCCAA | | | | |
| MHV N | (466) | GCGGACACCAATAACCGCTCTGATATTGTCGAAAGGGAGCCAA | | | | |
| Avian infectious bronchitis N | (361) | GCTGATGTGAAATCTAGATCCAAACAGGGTACTAGAGATCCTG | | | | |
| Consensus | (474) | GCTGATGTCAATACCCG TCTGACATTGTGATAGGGAGCCAA | | | | |
| | | | | | | Section 13 |
| | (517) | 517 | 530 | 540 | | 559 |
| BCV N | (500) | GTAGCGATGAGGCTATTCCGACTA-GGTTTCGGCCTGGCACGG | | | | |
| MHV N | (509) | GCAGTCATGAGGCTATTCCACTA-GGTTTGCGCCCGGCACGG | | | | |
| Avian infectious bronchitis N | (404) | ATAAGTTTGAT-CAATACCCACTACGGTTTTCAGATGG----- | | | | |
| Consensus | (517) | GTAG ATGAGGCTATTCC ACTA GGTTT CGCCTGGCACGG | | | | |
| | | | | | | Section 14 |
| | (560) | 560 | 570 | 580 | 590 | 602 |
| BCV N | (542) | TACTCCCTCAGGGTTACTATATTGAAGGCTCAGGAAGGTCTGC | | | | |
| MHV N | (551) | TATTGCCTCAGGGCTTTTATGTTGAAGGCTCTGGAAGGTCTGC | | | | |
| Avian infectious bronchitis N | (441) | -AGGACCTGATGGTAATT-----TCCGTTGGGACTTC | | | | |
| Consensus | (560) | TA T CCTCAGGGTTATTAT TTGAAGGCTC GGAAGGTCTGC | | | | |

FIGURE 3A (contd.)

Section 15

| | | | | | | |
|-------------------------------|-------|--|-----|-----|-----|-----|
| | (603) | 603 | 610 | 620 | 630 | 645 |
| BCV N | (585) | TCCTAATTCCAGATCTACTTCACGCGCA---TCCAGTAGAGCC | | | | |
| MHV N | (594) | ACCTGCTAGCCGATCTGGTTCCGCGGTACCAATCCCGTGG-GCC | | | | |
| Avian infectious bronchitis N | (472) | AT-TCCTCTGAGTCGTGGTAGGAGTGGAGATCAACCCGAGCA | | | | |
| Consensus | (603) | ACCT CT CAGATCTGGTTCGCG GCA ATCCAGTGGAGCC | | | | |

Section 16

| | | | | | |
|-------------------------------|-------|--|-----|-----|-----|
| | (646) | 646 | 660 | 670 | 688 |
| BCV N | (625) | TCTAGTGCAGGATCGCGTAGTAGAGCCAATTCTGGCAACAGAA | | | |
| MHV N | (636) | AAATA-----ATCGCG--CTAGAAGCAGTTCCAACCCAGCGCC | | | |
| Avian infectious bronchitis N | (514) | TCATCAGCGGCATCTAG---TAGAGTACCAATCCCGTGAGGGTT | | | |
| Consensus | (646) | TCAT GC G ATCGCG TAGAG CA TTCC GC AG G | | | |

Section 17

| | | | | | | |
|-------------------------------|-------|--|-----|-----|-----|-----|
| | (689) | 689 | 700 | 710 | 720 | 731 |
| BCV N | (668) | CCCCCTACCTCTGGTGTAACACCTGATATGGCTGATCAAATTGC | | | | |
| MHV N | (671) | AGCCCTGGCTCTACTGTAAACCTGATATGGCCGAAGAAATTGC | | | | |
| Avian infectious bronchitis N | (554) | CAGGTGGTCGTAGGAGTGGAGCTGA---AGATGATCTGATTGC | | | | |
| Consensus | (689) | C CCTGCCTCTAGTGTA ACCTGATATGGCTGATCAAATTGC | | | | |

Section 18

| | | | | | | |
|-------------------------------|-------|---|-----|-----|-----|-----|
| | (732) | 732 | 740 | 750 | 760 | 774 |
| BCV N | (711) | TAGTCTTGTTCTGCGAAAACTTGGCAAGGATGCCACTAAGCCA | | | | |
| MHV N | (714) | TGCTCTTGTTTGGCTAAGCTCGGTAAAGATGCCGGCCAGCCC | | | | |
| Avian infectious bronchitis N | (594) | CCGTGCAGCAAAGATTATTGAGCACCAGCAG---AGGAAGGGT | | | | |
| Consensus | (732) | T GTCTTGTT TGGCTAA CT GGCAAGGATGCCAG AAGCC | | | | |

Section 19

| | | | | | | |
|-------------------------------|-------|--|-----|-----|-----|-----|
| | (775) | 775 | 780 | 790 | 800 | 817 |
| BCV N | (754) | CAGCAAGTAAGTAAGCAGACTGCCAAAGAAATCAGACA--GAA | | | | |
| MHV N | (757) | AAGCAAGTAAGGAAGCAAAGTGCCAAAGAAGTCAGGCA--GAA | | | | |
| Avian infectious bronchitis N | (634) | ACGCGCATTACTAAGCAAAAGGCAGAAAGAGATGGCTCATCCCC | | | | |
| Consensus | (775) | AAGCAAGTAAGTAAGCAA TGCCAAAGAAATCAG CA GAA | | | | |

Section 20

| | | | | | | |
|-------------------------------|-------|--|-----|-----|-----|-----|
| | (818) | 818 | 830 | 840 | 850 | 860 |
| BCV N | (795) | AATTTTGAATAAGCCCCGCCAGAGAGAGCCCCAATAAACA | | | | |
| MHV N | (798) | AATTTTAAACAAGCCTCGCCAAAAGAGGACTCCAACAAGCAG | | | | |
| Avian infectious bronchitis N | (677) | GATTCTGTAAAGCGTACGGTGCCACCAGGTTATAGAGTAGATCA | | | | |
| Consensus | (818) | AATTTTGA AAGCCCCGCCA AAGAGGA CC AATAAACA | | | | |

Section 21

| | | | | | | |
|-------------------------------|-------|--|-----|-----|-----|-----|
| | (861) | 861 | 870 | 880 | 890 | 903 |
| BCV N | (838) | TGCACGTGTCAGCAGTGTTTTGGGAAGAGAGGCCCAATCAGA | | | | |
| MHV N | (841) | TGCCAGTGTCAGCAGTGTTTTGGAAAGAGAGGCCCAATCAGA | | | | |
| Avian infectious bronchitis N | (720) | AGTTTTTGCCCTCGTACTAAAGGTAAAGAGGGT-----A | | | | |
| Consensus | (861) | TGC CTGTGCAGCAGTGTTTTGGGAAGAGAGGCCCAATCAGA | | | | |

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FIGURE 3A (contd.)

Section 22

| | (904) | 904 | 910 | 920 | 930 | 946 |
|-------------------------------|-------|--|-------------------------------|-----|-----|-----|
| BCV N | (881) | ATTTTGGTGGTGGGAGAAATGTTAAAACTTGGAACTAGTGACCC | | | | |
| MHV N | (884) | ATTTTGGAGGCTCTGAAATGTTAAAACTTGGAACTAGTGATCC | | | | |
| Avian infectious bronchitis N | (755) | ATTTTGGTGTATGACAAGATGAATGAGGAAGGTATTAAGGATGG | | | | |
| Consensus | (904) | ATTTTGGTGGTG | GAAATGTTAAAACTTGGAACTAGTGATCC | | | |

Section 23

| | (947) | 947 | 960 | 970 | 989 |
|-------------------------------|-------|--|-----------------------|-----|-----|
| BCV N | (924) | ACAGTTCCCCATTCTTGCAGAAC | -TCGCACCCACAGCTGGTGCC | | |
| MHV N | (927) | ACAGTTCCCCATTCTTGCAGAGT | -TGGGTCCAACAGTTGGTGCC | | |
| Avian infectious bronchitis N | (798) | GC-GTGTACAGCAATGCTCAACCTTACACCAAGCCGACATGC | | | |
| Consensus | (947) | ACAGTTCCCCATTCTTGCAGAAC | TGCACCAACAGCTGGTGCC | | |

Section 24

| | (990) | 990 | 1000 | 1010 | 1020 | 1032 |
|-------------------------------|-------|--|------------|------------|-------|------|
| BCV N | (966) | GTTCCTTTCTTGGATCAAGATTAGAGTTGGCCAAAGTGCAGAAT | | | | |
| MHV N | (969) | CTTCCTTCTTTGGATCTAAATTAGAATTTGGTCAAAA | ---AGAAT | | | |
| Avian infectious bronchitis N | (840) | TGTCTTTTGGAGTAGAGT | -GAC | ---GCCCAAG | ----- | |
| Consensus | (990) | TTTTTCTTTGGATCTAGATTAGA | TTGGCCAAAG | AGAAT | | |

Section 25

| | (1033) | 1033 | 1040 | 1050 | 1060 | 1075 |
|-------------------------------|--------|--|--------------------|-------|---------|------|
| BCV N | (1009) | TTGTCTGGGAATCTTGCAGAGCCCCAGAAAGGATGTTTATGAAT | | | | |
| MHV N | (1009) | T---CTGGTGGTGGCTGATGAACCCACCAAGATGTGTATGAGC | | | | |
| Avian infectious bronchitis N | (871) | ----CT--TCACACAGATGGGCTTC | ---ACCTTAGATTGGAAT | | | |
| Consensus | (1033) | TCTGGTATCCTGATGAGCCCC | AA | GATGT | TATGAAT | |

Section 26

| | (1076) | 1076 | 1090 | 1100 | 1118 |
|-------------------------------|--------|--|-----------------------------|------------------|---------|
| BCV N | (1052) | TGCGCTATAATGGTGCAATTAGATTTGACAGTACACTTTTCAGG | | | |
| MHV N | (1049) | TGCAATATTTCAGGTGCAGTTAGATTTGATAGTACTCTACCTGC | | | |
| Avian infectious bronchitis N | (905) | TT-ACTACTGGGTGGC | --TAGAGATGACCCGCAAGTTTGATAA | | |
| Consensus | (1076) | TGCACTATT | TGGTGCA | TTAGATTTGACAGTAC | CTTCTGG |

Section 27

| | (1119) | 1119 | 1130 | 1140 | 1150 | 1161 |
|-------------------------------|--------|--|-------------------------------|-------|----------------------|------|
| BCV N | (1095) | TTTGTAGACCATA | ---ATGAAGGTGTTGAATGAGAATTTGAA | | | |
| MHV N | (1092) | TTTGTAGACTATC | ---ATGAAAGTGTGAATGAGAATTTGAA | | | |
| Avian infectious bronchitis N | (945) | TTATGTAAAAATTTGTGATGAGTGTGTTGATGCTGTAG | ---GAA | | | |
| Consensus | (1119) | TTTGTAGAC | AT | ATGAA | GTGTTGAATGAGAATTTGAA | |

Section 28

| | (1162) | 1162 | 1170 | 1180 | 1190 | 1204 | |
|-------------------------------|--------|----------------------------------|---------------------|--------------|--------|------|--------|
| BCV N | (1134) | TGCATATCAACAACAAGATGGTAT | -GATGAATATGA | -GTCCAA | | | |
| MHV N | (1131) | TGCTTACCAGAAGGATGGTGGTGCAGATGTGG | -TGA | -GCCCAA | | | |
| Avian infectious bronchitis N | (986) | CACGTCCAAAGGACGAAGTTGTAA | -GACCAAAGTCACGCCCAA | | | | |
| Consensus | (1162) | TGC | TACCAA | AACAAGGTGGTA | GATGAA | TGA | GCCCAA |

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FIGURE 3A (contd.)

| | | | | | | Section 29 |
|--------------------------------------|--------|---|------|--------------------------|------------------|---------------|
| | (1205) | 1205 | 1210 | 1220 | 1230 | 1247 |
| BCV N (1175) | | AACCACAGCGTCA | --- | GCGTGGTGAG | --- | AAGAATGGACAAG |
| MHV N (1172) | | AGCCCCAAAGAAAAGGGCGTAGACAGGCTCAGGAAAAGA | -AAG | | | |
| Avian infectious bronchitis N (1028) | | ATTCAAGACCTGC | -- | TACAAGAACAAAG | -TTCTCCAGCGCCAAG | |
| Consensus (1205) | | A CCACAACGT A | | GCGTGGACAGG T A | GAA GACAAG | |
| | | | | | | Section 30 |
| | (1248) | 1248 | 1260 | 1270 | 1280 | 1290 |
| BCV N (1211) | | GAGAAAATGATAATATAAGTGTTCAGCGCCTAAAAGCCGTGT | | | | |
| MHV N (1214) | | ATGAAGTAGATAATGTAAGCGTTGCAAAGCCCAAAGCTCTGT | | | | |
| Avian infectious bronchitis N (1068) | | ACAAACAGCGTCAAAGGAAGGAGAAGAGTCAAAGAAGCAGGAT | | | | |
| Consensus (1248) | | A GAAA GATAATATAAG GTTGCAA GCC AAAAGC GTGT | | | | |
| | | | | | | Section 31 |
| | (1291) | 1291 | 1300 | 1310 | 1320 | 1333 |
| BCV N (1254) | | GCAGCAAAATAAGAGTAGACAGTTGACTGCAGA | --- | GGACATC | | |
| MHV N (1257) | | GCAGCGAAATGTAAGTAGAGAATTAAACCCAGA | --- | GGATAGA | | |
| Avian infectious bronchitis N (1111) | | GATGAAGTAGATAAG | --- | GCATTGACCTCAGATGAGGAGAGG | | |
| Consensus (1291) | | GCAGCAAAATATAAGTAGAGAATTGACC CAGA | | GGA AG | | |
| | | | | | | Section 32 |
| | (1334) | 1334 | 1340 | 1350 | 1360 | 1376 |
| BCV N (1294) | | AGCCTTCT | --- | TAACAAGATGGATGA | --- | GCCCTATA |
| MHV N (1297) | | AGTCTGTTGGCTCAGATCCTTGATGATGCGTAGTGCCAGATG | | | | |
| Avian infectious bronchitis N (1150) | | AACAATGCACAGCTGGAATTTGATGATGAACCCAAGGTGATTA | | | | |
| Consensus (1334) | | AGCCTT T TCAGAA TTGATGATG | | GCC ATA | | |
| | | | | | | Section 33 |
| | (1377) | 1377 | 1390 | 1400 | | 1414 |
| BCV N (1325) | | CT | --- | GAAGACACCTCAGAAATATAA | --- | |
| MHV N (1340) | | GGTTAGAAGATGACTCTAATGTGTAA | --- | | | |
| Avian infectious bronchitis N (1193) | | ACTGGGGGGATTTCAGCACTTGGAGAGAATGAGTTGTAA | | | | |
| Consensus (1377) | | T GAAGAT CCTCA ATGTATAA | | | | |
| BCV N | | SEQ ID NO: 9883 | | | | |
| MHV N | | SEQ ID NO: 9894 | | | | |
| Avian infectious bronchitis N | | SEQ ID NO: 9903 | | | | |

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FIGURE 3B

| Section 1 | | | | | | |
|------------------------------------|-------|--|-----|-----|-----|-----|
| | (1) | 1 | 10 | 20 | 30 | 41 |
| HOBMPRO | (1) | GATGTGGATGACGTTT | | | | |
| BCV M | (1) | -----ATGAGTAGT | | | | |
| MHV M | (1) | -----ATGACTAGT | | | | |
| Avian infectious brochitis virus M | (1) | ----- | | | | |
| Consensus | (1) | ATGAGTAGT | | | | |
| Section 2 | | | | | | |
| | (42) | 42 | 50 | 60 | 70 | 82 |
| HOBMPRO | (42) | AAAACCTA---CTCCAGCACCAGTTTATATCTGGAGTGCTGA | | | | |
| BCV M | (10) | GTAACCTA---CACCAGCACCAGTTTACACCTGGACTGCTGA | | | | |
| MHV M | (10) | ACCACTCAGGCTCCACAGCCTGTTTATCAGTGGACGGCTGA | | | | |
| Avian infectious brochitis virus M | (1) | --ATGTC---GAA CGCGCAAATTGCACCTCTGACTG-TGA | | | | |
| Consensus | (42) | A AACTC CTCCAGCGCCAGTTTATCTCTGGACTGCTGA | | | | |
| Section 3 | | | | | | |
| | (83) | 83 | 90 | 100 | 110 | 123 |
| HOBMPRO | (80) | TGAAGCTATTAAATTCCTAAAGGAATGGAATTTTCTTTTGG | | | | |
| BCV M | (48) | TGAAGCTATTAAATTCCTAAAGGAATGGAACITTTCTTTTGG | | | | |
| MHV M | (51) | TGAGGCAATTCGATTCCCTTAAGGAATGGAATTTCTCTCTCG | | | | |
| Avian infectious brochitis virus M | (36) | ACAGTCAGTTGAGCTTTTAAAGAAATATAATTTATTATATAA | | | | |
| Consensus | (83) | TGAGGCTATTAAATTCCTTAAGGAATGGAATTTTCTTTTGG | | | | |
| Section 4 | | | | | | |
| | (124) | 124 | 130 | 140 | 150 | 164 |
| HOBMPRO | (121) | GTATTATACTACTTTTTATTACAAATCATATTGCAATTTTGG | | | | |
| BCV M | (89) | GTATTATACTACTTTTTATTACAAATCATATTGCAATTTTGG | | | | |
| MHV M | (92) | GCATTATACTACTTTTTGTTACTATCATACTACAGTTCCGTT | | | | |
| Avian infectious brochitis virus M | (77) | CCGCATTCCCTATTGTTTCTTACTATACTACTTCAGTATGGA | | | | |
| Consensus | (124) | GTATTATACTACTTTTTATTACTATCATATTGCAGTTTGG | | | | |
| Section 5 | | | | | | |
| | (165) | 165 | 170 | 180 | 190 | 205 |
| HOBMPRO | (162) | TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT | | | | |
| BCV M | (130) | TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT | | | | |
| MHV M | (133) | TACACGAGCCGTAGCATGTTTGTTTATGTTTGGAATGAT | | | | |
| Avian infectious brochitis virus M | (118) | TATGCAACAAGGAGTCGGTTTATTACATAATGAAATGAT | | | | |
| Consensus | (165) | TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT | | | | |
| Section 6 | | | | | | |
| | (206) | 206 | 220 | 230 | 246 | |
| HOBMPRO | (203) | TATTTTGTGGCTTATGTGGCCCCCTTACTATAATCTTAACTA | | | | |
| BCV M | (171) | CATTTTGTGGCTTATGTGGCCCCCTTACTATCATCTTAACTA | | | | |
| MHV M | (174) | ACTTTTGTGGCTTATGTGGCCACTAACTATTGTTTGTGTA | | | | |
| Avian infectious brochitis virus M | (159) | AGTGTATGCTGCTTTTGGCCCCCTTAAACATTGCAGTAGGTG | | | | |
| Consensus | (206) | AATTTTGTGGCTTATGTGGCCCCCTTACTATTGTCTTAACTA | | | | |

FIGURE 3B (contd.)

| | | | | | | |
|--|--|-----|-----|-----|-----|-----|
| Section 7 | | | | | | |
| | (247) | 247 | 260 | 270 | 287 | |
| HOBMPRO (244) | TTTTCAATTGCGTATACGCATTGAATAATGTGTATCTTGGC | | | | | |
| BCV M (212) | TTTTCAATTGCGTGTATGCGTTGAATAATGTGTATCTTGGC | | | | | |
| MHV M (215) | TTTTTAAC TGCGTCTATGCGCTAAATAATGTGTATCTTGGA | | | | | |
| Avian infectious brochitis virus M (200) | TAATTTCAATGTATATATCCACCAAATACAGGAGGTCTTGTC | | | | | |
| Consensus (247) | TTTTTAATTGCGTATATGCGTTGAATAATGTGTATCTTGGC | | | | | |
| Section 8 | | | | | | |
| | (288) | 288 | 300 | 310 | 328 | |
| HOBMPRO (285) | CTTCTATAGTTTTTACCATAGTGGCCATTATTATGTGGAT | | | | | |
| BCV M (253) | TTTTCTATAGTTTTCACATAGTGGCCATTATCATGTGGAT | | | | | |
| MHV M (256) | TTTTCTATAGTGTTTTACTATAGTGTCCATTATAATGTGGAT | | | | | |
| Avian infectious brochitis virus M (241) | GCAGCGAAAATACTTACAGTGGTTGCGTGTCTGTCTTTTGA | | | | | |
| Consensus (288) | TTTTCTATAGTTTTTACTATAGTGGCCATTAT ATGTGGAT | | | | | |
| Section 9 | | | | | | |
| | (329) | 329 | 340 | 350 | 369 | |
| HOBMPRO (326) | TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAAGCTG | | | | | |
| BCV M (294) | TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAAGCTG | | | | | |
| MHV M (297) | TATGTATTTTGTGAATAGCATCAGGTTGTTTATCAGGACTG | | | | | |
| Avian infectious brochitis virus M (282) | AGGATATTGGATTTCAGAGTATCAGACTCTTTAAGCGGGGTG | | | | | |
| Consensus (329) | TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGGACTG | | | | | |
| Section 10 | | | | | | |
| | (370) | 370 | 380 | 390 | 400 | 410 |
| HOBMPRO (367) | GAAGTTTTTGGAGTTTCAACCCAGAAACAAACAACCTTGATG | | | | | |
| BCV M (335) | GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACCTTGATG | | | | | |
| MHV M (338) | GCAGCTGGTGGAGCTTCAACCCGAAACAAACAACCTTAATG | | | | | |
| Avian infectious brochitis virus M (323) | GGCAATGGTGGGCATTTAACCOCTGAGTCTAA-----TGCCG | | | | | |
| Consensus (370) | GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACCTTGATG | | | | | |
| Section 11 | | | | | | |
| | (411) | 411 | 420 | 430 | 440 | 451 |
| HOBMPRO (408) | TGTATAGATATGAAAGGAACAATGTATGTTAGGCCGATAAT | | | | | |
| BCV M (376) | TGTATAGATATGAAAGGAAGGATGTATGTTAGGCCGATAAT | | | | | |
| MHV M (379) | TGTATAGATATGAAAGGTACTGTGTATGTTAGACCCATTAT | | | | | |
| Avian infectious brochitis virus M (359) | T-----AGGT-TCAATACTCCTATCTA-----ATGGTCAACAAT | | | | | |
| Consensus (411) | TGTATAGATATGAAAGGTACTATGTATGTTAGGCCGATAAT | | | | | |
| Section 12 | | | | | | |
| | (452) | 452 | 460 | 470 | 480 | 492 |
| HOBMPRO (449) | TGAGGACTATCATACTCTGACGGTCACAATAATACGCGGCC | | | | | |
| BCV M (417) | TGAGGACTAGCATACCCCTTACGGTCACAATAATACGTGGTC | | | | | |
| MHV M (420) | AGAGGATTACCATACACTAACAGCCACTATCATTCGTGGTC | | | | | |
| Avian infectious brochitis virus M (392) | GTAATTTTGTATAGA--GAGTGTGCCAAT-----GGTG | | | | | |
| Consensus (452) | TGAGGATTACCATACACTGACGGTCACAATAATACGTGGTC | | | | | |

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FIGURE 3B (contd.)

| | | | | | | |
|--|-------|---|-----|-----|-----|-----|
| Section 13 | | | | | | |
| | (493) | 493 | 500 | 510 | 520 | 533 |
| HOBMPRO (490) | | ATGTTTACATTCAAGGTATAAACTAGGTACTGGCTATTCT | | | | |
| BCV M (458) | | ATCTTTACATGCAAGGTATAAACTAGGTACTGGCTATTCT | | | | |
| MHV M (461) | | ACCTCTATATGCAAGGTGTTAAGCTAGGCACCTGGCTTCTCT | | | | |
| Avian infectious brochitis virus M (424) | | CTTTCT - - - - CCAATTATAAAGAATGGAGTTCTTTATTGT | | | | |
| Consensus (493) | | ATCTTTACATGCAAGGTATAAAGCTAGGTACTGGCTATTCT | | | | |
| Section 14 | | | | | | |
| | (534) | 534 | 540 | 550 | 560 | 574 |
| HOBMPRO (531) | | TGGGCAGATTTGCCAGCTTATATGACTGTTGCTAAGGTTAC | | | | |
| BCV M (499) | | TTGTCAGATTTGCCAGCTTATGTGACTGTTGCTAAGGTTCTC | | | | |
| MHV M (502) | | TTGTCCTGATTTGCCCTGCTTATGTTACAGTTGCTAAGGTTGTC | | | | |
| Avian infectious brochitis virus M (460) | | GAGGGTCAGTGGCTTGC - - - - TAAATGTGAACCAGACCAC | | | | |
| Consensus (534) | | TTGTCCTGATTTGCCCTGCTTATGTGACTGTTGCTAAGGTTCTC | | | | |
| Section 15 | | | | | | |
| | (575) | 575 | 580 | 590 | 600 | 615 |
| HOBMPRO (572) | | ACACCTGTGCACATATAAGCGTGGTTTTCTTGACAGGATAA | | | | |
| BCV M (540) | | ACACCTGCTCAAGTATAAGCGTGGTTTTCTTGACAAGATAG | | | | |
| MHV M (543) | | TCACCTTTGCACTTATAAGCGCGCATTTCTTAGACAAGGTAG | | | | |
| Avian infectious brochitis virus M (496) | | TTGCCATAAAGACATATTTG - - - - - TTGCCCCACCAGATAG | | | | |
| Consensus (575) | | TCACCTGTGCACATATAAGCGTGGTTTTCTTGACAAGATAG | | | | |
| Section 16 | | | | | | |
| | (616) | 616 | 630 | 640 | | 656 |
| HOBMPRO (613) | | GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC | | | | |
| BCV M (581) | | GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC | | | | |
| MHV M (584) | | ACGGTGTTAGCGGTTTTGCTGTTTATGTTAAGTCCAAAGTC | | | | |
| Avian infectious brochitis virus M (531) | | ACG-TAATA - - - - - TCTACCGTATG-GTGCAG - - - AAATAG | | | | |
| Consensus (616) | | GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC | | | | |
| Section 17 | | | | | | |
| | (657) | 657 | 670 | 680 | | 697 |
| HOBMPRO (654) | | GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT | | | | |
| BCV M (622) | | GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT | | | | |
| MHV M (625) | | GGAAATTACCGACTGCCCTCAAAATAAACCGAGT - - - GGCAT | | | | |
| Avian infectious brochitis virus M (562) | | ACTGGTGACC - AAAGCGGAAATAAGAAAAGGTTTGCTACA- | | | | |
| Consensus (657) | | GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT | | | | |
| Section 18 | | | | | | |
| | (698) | 698 | 710 | 720 | | 738 |
| HOBMPRO (695) | | GGACACCGCATTGTTGAGAAATAATATCTAAATTTTAAGGA | | | | |
| BCV M (663) | | GGACACCGCATTGTTGAGAAATAATATCTAA - - - - - | | | | |
| MHV M (663) | | GGACACCGCATTGTTGAGA - - - - - ATCTAA - - - - - | | | | |
| Avian infectious brochitis virus M (601) | | - - - - - | | | | |
| Consensus (698) | | GGACACCGCATTGTTGAGAAATAATATCTAA | | | | |
| Section 19 | | | | | | |
| | (739) | | | | | |
| HOBMPRO (736) | TG | SEQ ID NO: 9912 | | | | |
| BCV M (694) | -- | SEQ ID NO: 9884 | | | | |
| MHV M (688) | -- | SEQ ID NO: 9895 | | | | |
| Avian infectious brochitis virus M (601) | -- | SEQ ID NO: 9904 | | | | |
| Consensus (739) | | | | | | |

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FIGURE 3C

| | | | | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|-----|-----------|--|
| | | | | | | | | Section 1 | |
| | (1) | 1 | 10 | 20 | 30 | 40 | 53 | | |
| HOBHEGA | (1) | CTAAACTCAGTGAAAATGTTTTTGGCTTCCTAGATTTATTCTAGTTAGCTGCAT | | | | | | | |
| BCV HE | (1) | CTAAACTCAGTGAAAATGTTTTTGGCTTCCTAGATTTGTTCTAGTTAGCTGCAT | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (1) | CTAAACTCAGTGAAAATGTTTTTGGCTTC TAGATTT TTCTAGTTAGCTGCAT | | | | | | | |
| | | | | | | | | Section 2 | |
| | (54) | 54 | 60 | 70 | 80 | 90 | 106 | | |
| HOBHEGA | (54) | AATTGGTAGCTTAGGTTTTTACAACCTCCTACCAATGTTGTTTCGCATGTAA | | | | | | | |
| BCV HE | (54) | AATTGGTAGCCTTAGGTTTTTGACAATCCTCCTACCAATGTTGTTTCGCATTTAA | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (54) | AATTGGTAGC TAGGTTTT ACAA CCTCCTACCAATGTTGTTTCGCAT TAA | | | | | | | |
| | | | | | | | | Section 3 | |
| | (107) | 107 | 120 | 130 | 140 | | 159 | | |
| HOBHEGA | (107) | ATGGAGATTGGTTTTTATTGTTGACAGTCGTTTCAGATTGTAATCATATTGTT | | | | | | | |
| BCV HE | (107) | ATGGAGATTGGTTTTTATTGTTGACAGTCGTTTCAGATTGTAATCATATTGTT | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (107) | ATGGAGATTGGTTTTTATTGTTGACAGTCGTTTCAGATTGTAATCAT TTGTT | | | | | | | |
| | | | | | | | | Section 4 | |
| | (160) | 160 | 170 | 180 | 190 | 200 | 212 | | |
| HOBHEGA | (160) | AATATCAACCCCCATAATTATTCTTATATGGACCTTAATCCTCTTCTGTGTGA | | | | | | | |
| BCV HE | (160) | ACTACCAACCCCGCGTAATTATTCTTATATGGACCTTAATCCTGCTTGTGTGG | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (160) | A TA CAACCCCC TAATTATTCTTATATGGACCTTAATCCTG TGTGTG | | | | | | | |
| | | | | | | | | Section 5 | |
| | (213) | 213 | 220 | 230 | 240 | 250 | 265 | | |
| HOBHEGA | (213) | TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT | | | | | | | |
| BCV HE | (213) | TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (213) | TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT | | | | | | | |
| | | | | | | | | Section 6 | |
| | (266) | 266 | 280 | 290 | 300 | | 318 | | |
| HOBHEGA | (266) | TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTTTTATGAG | | | | | | | |
| BCV HE | (266) | TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTTCTATGAG | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (266) | TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTT TATGAG | | | | | | | |
| | | | | | | | | Section 7 | |
| | (319) | 319 | 330 | 340 | 350 | 360 | 371 | | |
| HOBHEGA | (319) | GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA | | | | | | | |
| BCV HE | (319) | GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCACCACCTTCTGGTAGTAA | | | | | | | |
| MHV HE | (1) | ----- | | | | | | | |
| Consensus | (319) | GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCA C TTCTGGTAGTAA | | | | | | | |

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FIGURE 3C (contd.)

Section 8

| | | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|-----|
| | (372) | 372 | 380 | 390 | 400 | 410 | 424 |
| HOBHEGA | (372) | TGATATTTGGATGCAGAATAAAGGCTTGTTTTATACTCAGGTTTATAAGAATA | | | | | |
| BCV HE | (372) | TGATATTTGGATGCAGAATAAAGGCTTGTTTTACACTCAGGTTTATAAGAATA | | | | | |
| MHV HE | (1) | -----ATGGGCAATAAAGCTCGATTTTATGCCCCGAGTGTATGAGAAGA | | | | | |
| Consensus | (372) | TGATATTTGGATGCAGAATAAAGGCTTGTTTTATACTCAGGTTTATAAGAATA | | | | | |

Section 9

| | | | | | | | |
|-----------|-------|--|-----|-----|-----|-----|-----|
| | (425) | 425 | 430 | 440 | 450 | 460 | 477 |
| HOBHEGA | (425) | TGGCTGGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC | | | | | |
| BCV HE | (425) | TGGCTGGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC | | | | | |
| MHV HE | (44) | TGGCCCAATATAGGAGCCTATCGTTTGTTAATGTGTCTTATGCCCTATGGAGGT | | | | | |
| Consensus | (425) | TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC | | | | | |

Section 10

| | | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|-----|
| | (478) | 478 | 490 | 500 | 510 | 520 | 530 |
| HOBHEGA | (478) | TCTGCACAATCTACAGCCTTTGTAAATCTGGTAGTTTAGTCCTTAATAACCC | | | | | |
| BCV HE | (478) | TCTGCACAATCTACAGCCTTTGTAAATCTGGTAGTTTAGTCTTAATAAACCC | | | | | |
| MHV HE | (97) | AATGCACAAGCCCGCCTCCATTTGCAAGACAATACCTTAACACTCAATAACCC | | | | | |
| Consensus | (478) | TCTGCACAATCTACAGCCTTTGTAAATCTGGTAGTTTAGT CTTAATAACCC | | | | | |

Section 11

| | | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|-----|
| | (531) | 531 | 540 | 550 | 560 | 570 | 583 |
| HOBHEGA | (531) | TGCATATATAGCTCCTCAAGCTAACTCTGGGATTATTATTATAAGGTTGAAG | | | | | |
| BCV HE | (531) | TGCATATATAGCTCGTGAAGCTAATTTTGGGATTATTATTATAAGGTTGAAG | | | | | |
| MHV HE | (150) | CACCTTCATATCGAAGGAGTCTAATTATGTTGATTATTACTATGAGAGTGAAG | | | | | |
| Consensus | (531) | TGCATATATAGCTC TGAAGCTAATT TGGGATTATTATTATAAGGTTGAAG | | | | | |

Section 12

| | | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|-----|
| | (584) | 584 | 590 | 600 | 610 | 620 | 636 |
| HOBHEGA | (584) | CTGATTTTATTTTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT | | | | | |
| BCV HE | (584) | CTGATTTTATTTTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT | | | | | |
| MHV HE | (203) | CTAATTTTCACTAGAAAGGTTGTGATGAATTTATAGTACCGCTCTGTGGTTTT | | | | | |
| Consensus | (584) | CTGATTTTATTTTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT | | | | | |

Section 13

| | | | | | | |
|-----------|-------|---|-----|-----|-----|-----|
| | (637) | 637 | 650 | 660 | 670 | 689 |
| HOBHEGA | (637) | AACGGCAAGTTTTTG-----TCGAATACA-----AAGTATTATGATGA | | | | |
| BCV HE | (637) | AACGGCAAGTTTTTG-----TCGAATACA-----AAGTATTATGATGA | | | | |
| MHV HE | (256) | AATGGCCATTCCAAGGGCAGCTCTTCGGATGCTGCCAATAAATATTATACTGA | | | | |
| Consensus | (637) | AACGGCAAGTTTTTG TCGAATACA AAGTATTATGATGA | | | | |

Section 14

| | | | | | | | |
|-----------|-------|--|-----|-----|-----|-----|-----|
| | (690) | 690 | 700 | 710 | 720 | 730 | 742 |
| HOBHEGA | (675) | TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA | | | | | |
| BCV HE | (675) | TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA | | | | | |
| MHV HE | (309) | CTCTCAGAGTTACTATAATATGGATATGGTGTTCTTATATGGGTTCAATTCTA | | | | | |
| Consensus | (690) | TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA | | | | | |

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FIGURE 3C (contd.)

| Section 15 | | | | | | | |
|------------|--------|------|--|--|--------------------------|-----------------------|--------------|
| | (743) | 743 | 750 | 760 | 770 | 780 | 795 |
| HOBHEGA | (728) | C | -----AGAAACCATTACGA----- | ----- | CTGGTTTTGATCTTAATTGTTAT | | |
| BCV HE | (728) | C | -----TGAAACCATTACCA----- | ----- | CTGGTTTTGACTTTAAATTGTCAT | | |
| MHV HE | (362) | C | CTTG | GATGTTGGCAACACTGCTAAGGAT | CCGGGTCTTGATCTCACTTGCAGG | | |
| Consensus | (743) | C | | TGAAACCATTACCA | | CTGGTTTTGATCTTAATTGT | AT |
| Section 16 | | | | | | | |
| | (796) | 796 | 810 | 820 | 830 | 848 | |
| HOBHEGA | (766) | T | ATT | TAGTTTTACCCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT | | | |
| BCV HE | (766) | T | ATT | TAGTTCTACCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT | | | |
| MHV HE | (415) | T | ATCTTGCATTGACTCCTGGTAATTATAAGGCTGTGTCCTTAGAATATTTGTT | | | | |
| Consensus | (796) | T | ATT | TAGTTTTACCCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT | | | |
| Section 17 | | | | | | | |
| | (849) | 849 | 860 | 870 | 880 | 890 | 901 |
| HOBHEGA | (819) | A | ACTGTTCTTACGAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG | | | | |
| BCV HE | (819) | A | ACTGTTCTTACTAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG | | | | |
| MHV HE | (468) | A | AGCTTACCCTCAAAGGCTATTTGCCCTCCATAAGACAAAGCGCTTTATGCCCTG | | | | |
| Consensus | (849) | A | ACTGTTCTTAC | AAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG | | | |
| Section 18 | | | | | | | |
| | (902) | 902 | 910 | 920 | 930 | 940 | 954 |
| HOBHEGA | (872) | T | ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC | | | | |
| BCV HE | (872) | T | ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC | | | | |
| MHV HE | (521) | T | GCAGGTAGTTGACTCAAGGTGGAGTAGCATCCGCCAGTCAGACAATATGACC | | | | |
| Consensus | (902) | T | ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC | | | | |
| Section 19 | | | | | | | |
| | (955) | 955 | 960 | 970 | 980 | 990 | 1007 |
| HOBHEGA | (925) | G | CGGTTGCTTGTCAAGCTCCGTA | CTGTTATTTTCGTAATTC | TACTAGCAACTA | | |
| BCV HE | (925) | G | CAGTTGCTTGTCAACCCCGTACTGTTATTTTCGTAATTC | TACTAGCAATTA | | | |
| MHV HE | (574) | G | CTGCAGCCTGTCAAGCTGCCATATTGTTTCTTTTCGCANACATCTGCGAATTA | | | | |
| Consensus | (955) | G | C | TTGCTTGTCAACC | CCGTA | CTGTTATTTTCGTAATTC | TACTAGCAATTA |
| Section 20 | | | | | | | |
| | (1008) | 1008 | 1020 | 1030 | 1040 | 1050 | 1060 |
| HOBHEGA | (978) | T | GTTGGTGTTT | ---ATGATATTAATCATGGAGATGCTGGTTTTACTAGCATA | C | | |
| BCV HE | (978) | T | GTTGGTGTTT | ---ATGATATCAATCATGGGATGCTGGTTTTACTAGCATA | C | | |
| MHV HE | (627) | T | AGTGGTGGCACACATGATGCGCACCATGGTGATTTTCATTTCAAGGCAGTTAT | | | | |
| Consensus | (1008) | T | GTTGGTGTTT | ATGATAT | AATCATGG | GATGCTGGTTTTACTAGCATA | C |
| Section 21 | | | | | | | |
| | (1061) | 1061 | 1070 | 1080 | 1090 | 1100 | 1113 |
| HOBHEGA | (1028) | T | TAGTGGTTTTGTTATATAATTCACTTGTTTTTCGCAGCAAGGCGTTTTTAGG | | | | |
| BCV HE | (1028) | T | CAGTGGTTTTGTTATATGACTCACCTTGTTTTTCGCAGCAAGGCGTTTTTAGG | | | | |
| MHV HE | (680) | T | GTCTGGTTTTGTTATATAATGTTTCCTGTATTGCCAGCAGGGTGCATTTCTT | | | | |
| Consensus | (1061) | T | A | GTGGTTTTGTTATATAATTCACTTGTTTTTCGCAGCAAGGCGTTTTTAGG | | | |

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FIGURE 3C (contd.)

Section 22

| | (1114) | 1114 | 1120 | 1130 | 1140 | 1150 | 1166 |
|------------------|--------|--|------|------|------|----------------|------|
| HOBHEGA (1081) | | TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGTCCAC | | | | | |
| BCV HE (1081) | | TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGCOCTAC | | | | | |
| MHV HE (733) | | TATAATAAATGTTAGTTCCTCTTCCAGCCTATGGGTACGGTCATTGTCCAAC | | | | | |
| Consensus (1114) | | TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCC | | | | TATGGCAGATGTCC | AC |

Section 23

| | (1167) | 1167 | 1180 | 1190 | 1200 | 1219 |
|------------------|--------|--|------|------|------|------|
| HOBHEGA (1134) | | TGCTGCTGATATTAATAACCCCTGATTTACCCATTTGTGTGTATGATCCGCTAC | | | | |
| BCV HE (1134) | | TGCTGCTGATATTAATAACCCCTGATGTACCTATTTGTGTGTATGATCCGCTAC | | | | |
| MHV HE (786) | | GGCAGCTAACATTGGTTA --- TATGGCACCTGTTTGTATCTATGACCCCTCTCC | | | | |
| Consensus (1167) | | TGCTGCTGATATTAATAACCCCTGATGTACCTATTTGTGTGTATGATCCGCTAC | | | | |

Section 24

| | (1220) | 1220 | 1230 | 1240 | 1250 | 1260 | 1272 |
|------------------|--------|--|------|------|------|------|------|
| HOBHEGA (1187) | | CAGTTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT | | | | | |
| BCV HE (1187) | | CAATTATTTTGCTTGGCATTCTTTTGGGGTGTTGCGGTCATAATTATTGTAGTT | | | | | |
| MHV HE (836) | | CGGTCACTACTGCTAGGTGTGTTATTGGGTATAGCTGTGTGATTATTGTGTTT | | | | | |
| Consensus (1220) | | CAGTTATTTTGCTTGGCATTCTTTTGGGTGTTGCGGTCATAATTATTGTAGTT | | | | | |

Section 25

| | (1273) | 1273 | 1280 | 1290 | 1300 | 1310 | 1325 |
|------------------|--------|---|------|------|------|------|------|
| HOBHEGA (1240) | | TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC | | | | | |
| BCV HE (1240) | | TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC | | | | | |
| MHV HE (889) | | TTGATGTTTATTTTATGACCGATAGCGGTGTTAGATTGCATGAGGCATAA-- | | | | | |
| Consensus (1273) | | TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC | | | | | |

Section 26

| | (1326) | 1326 | 1337 | |
|------------------|--------|--------------|------|-----------------|
| HOBHEGA (1293) | | CATAATCTAAAC | | SEQ ID NO: 9913 |
| BCV HE (1293) | | CATAATCTAAAC | | SEQ ID NO: 9885 |
| MHV HE (940) | | ----- | | SEQ ID NO: 9896 |
| Consensus (1326) | | CATAATCTAAAC | | |

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FIGURE 4**FIGURE 4A**

| | | Section 1 | | | |
|-------------------------------------|-------|--|-----|-----|-----|
| | | (1) 1 | 10 | 20 | 39 |
| avian infectious bronchitis pol 1ab | (1) | ----- | | | |
| bovine coronavirus pol 1ab | (1) | MSKINIKYGLLELHWAFEPFWMFEDAEELKLDNPSSEVDIV | | | |
| Human corona 229E pol 1ab | (1) | -----MACNRVTTLAVASDSEISANG | | | |
| Murine hepatitis pol 1ab | (1) | MAKMGKYGLGFKWAFEPFWMFLPNASEKLGNEPERSHEEDGF | | | |
| Consensus | (1) | MAKI KYGL WAFEPFWM NA EKL NPDSSSE D | | | |
| | | Section 2 | | | |
| | | (40) 40 | 50 | 60 | 78 |
| avian infectious bronchitis pol 1ab | (1) | ----- | | | |
| bovine coronavirus pol 1ab | (40) | CSTTAQKLETGGICPENHVMMDCRRLLKQEGCVQSSLEIR | | | |
| Human corona 229E pol 1ab | (21) | CSTIAQAVRRYSEAAASNGFRACRFVSLDLDQCIIVGIADD | | | |
| Murine hepatitis pol 1ab | (40) | GPSAAQEPKVKCKTLVNHVRVNC SRLPALECCVQSATIR | | | |
| Consensus | (40) | CST AQ LK G NHVRV C RLL LECCVQSATIR | | | |
| | | Section 3 | | | |
| | | (79) 79 | 90 | 100 | 117 |
| avian infectious bronchitis pol 1ab | (1) | ----- | | | |
| bovine coronavirus pol 1ab | (79) | ETVMNTRPYDLEVLLODAIOSREAVLVTEPLGMSIEACY | | | |
| Human corona 229E pol 1ab | (60) | TYVMGLHGNOTLFCNIMKFSDRPFMLHG-----WLVTIS | | | |
| Murine hepatitis pol 1ab | (79) | LTFVDEDEPKVLEASTMMALQFGSAVLVLPFSKRLSTQAWT | | | |
| Consensus | (79) | DIVM PN LE IMAIQ R AVL V P LSI AFS | | | |
| | | Section 4 | | | |
| | | (118) 118 | 130 | 140 | 156 |
| avian infectious bronchitis pol 1ab | (1) | ----MASSLKQGVSPK-----PRDVILVSKDI | | | |
| bovine coronavirus pol 1ab | (118) | VRCCNENGWMTMGLFRRRSVCNTGRCAVNKHVAYOLYIMID | | | |
| Human corona 229E pol 1ab | (93) | NSNYLLEEDVVFGR-----GGGNVTYTDQYLCGADG | | | |
| Murine hepatitis pol 1ab | (118) | NLGVLPKTAAMGLFKRVCLCNTRECS CDAHVVAEHLFTVQ | | | |
| Consensus | (118) | N G LP SF MGLFKR LCNTG CAV HVAYLLF D | | | |
| | | Section 5 | | | |
| | | (157) 157 | 170 | 180 | 195 |
| avian infectious bronchitis pol 1ab | (24) | PEQLCDALFFYTSHNPKDYADAEAVRQKFDRSLQTGKQF | | | |
| bovine coronavirus pol 1ab | (157) | PAGVCEGAGQFVGWVIFPLAFMPVOSKFFVPEWVMYLRKC | | | |
| Human corona 229E pol 1ab | (126) | KPVMSIDLWQFVDHEGENEETIINGHTYVCAWLTKRKPL | | | |
| Murine hepatitis pol 1ab | (157) | PDGVCLGNGRFLGWFEVPTAIREYAKOWLQPMSTLLRKG | | | |
| Consensus | (157) | PDGVCDGLGQFVGWFIPL AIPINARQFI PWLI LKK | | | |
| | | Section 6 | | | |
| | | (196) 196 | 210 | 220 | 234 |
| avian infectious bronchitis pol 1ab | (63) | KFET-----VC--CLFLILKGVDPKITPGVPAKV | | | |
| bovine coronavirus pol 1ab | (196) | GEKG-AYNKDHKRGGFHVYNFKVEDAYDLVHDEPKGKE | | | |
| Human corona 229E pol 1ab | (165) | DKKR-----Q--NNLATEETIEMHGDAHLTLR | | | |
| Murine hepatitis pol 1ab | (196) | GNKGSVTSGHFRRAVTMPVYDFNVEDACEEVHLNPKGKY | | | |
| Consensus | (196) | GFKG KRA M VYNL VEDA DLVHDAPKGKF | | | |

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FIGURE 4A (contd.)

| Section 7 | | | | | | |
|-------------------------------------|-------|--|-----|-----|-----|-----|
| | (235) | 235 | 240 | 250 | 260 | 273 |
| avian infectious bronchitis pol 1ab | (88) | LKATSKLADLEDIFGVSPILARKYRELLKTACQWSLTVEA | | | | |
| bovine coronavirus pol 1ab | (234) | SKKAYALIRGYRGVKPILLYVDQYGGDYTGGLADGLIAYYA | | | | |
| Human corona 229E pol 1ab | (190) | NGSVLEMAKEVKTSKVVLSDALDKLYKVFGSPVMTNGS | | | | |
| Murine hepatitis pol 1ab | (235) | SCKAYALLKGYRGVKPILFVDOYGGDYTGCLAKGLEDDYG | | | | |
| Consensus | (235) | SKKAYALAKGYRGVKPILLVDQYGCCLYTGA LA GLT YA | | | | |
| Section 8 | | | | | | |
| | (274) | 274 | 280 | 290 | 300 | 312 |
| avian infectious bronchitis pol 1ab | (127) | LDVRAQTLDEIFDPTTEILWLQVAAKIHVSSMAMRRRLVGE | | | | |
| bovine coronavirus pol 1ab | (273) | DKTLQEMKALFFIN SQEL PFDVTVAWHVVRDPRYVMRLQ | | | | |
| Human corona 229E pol 1ab | (229) | NILEAFTKPVFISALVQCTCGTKSWSVGDWTGFKSSCCN | | | | |
| Murine hepatitis pol 1ab | (274) | DITLSEMKELFPVWRDSL DSEVLVAWHVDRDPRRAAMRLQ | | | | |
| Consensus | (274) | DITLAETKDLFP I WSD L DV VAWHVDRDPRKAMRLQ | | | | |
| Section 9 | | | | | | |
| | (313) | 313 | 320 | 330 | 340 | 351 |
| avian infectious bronchitis pol 1ab | (166) | VTAKVMDALGSNLSALFQIVKQQTARI FOKALAI FENVN | | | | |
| bovine coronavirus pol 1ab | (312) | SASTIRSMAYVANPTEDLC DGSVVIKEPVHNYADDS EIL | | | | |
| Human corona 229E pol 1ab | (268) | VLSNKLQVVPGNV KPGDAVITTOQAGAGTRYFCGMTLKF | | | | |
| Murine hepatitis pol 1ab | (313) | TIATVRCIDYVCGPTEDVVDG DVVVRFAHLLAANATVK | | | | |
| Consensus | (313) | VIATVRCVLYVNQPTEDLV DGSVVAREPIKLLAA SIV | | | | |
| Section 10 | | | | | | |
| | (352) | 352 | 360 | 370 | 380 | 390 |
| avian infectious bronchitis pol 1ab | (205) | ELEFORIAALKMAEAKCARSLT VVVVERTLVVKEFAGTCL | | | | |
| bovine coronavirus pol 1ab | (351) | RQHNLYDIMS CFYMEADAVVNAFYGV DILKDCGFVMOEGY | | | | |
| Human corona 229E pol 1ab | (307) | VAN-----LEGVSVWRVTALQSVDC FVASSTEVE | | | | |
| Murine hepatitis pol 1ab | (352) | RLP---RLVETMLYTDSSVTEFCYKTKLCECGEITQEGY | | | | |
| Consensus | (352) | RLPN I IL FIEAASVI VIYL KL DCGFISQEGY | | | | |
| Section 11 | | | | | | |
| | (391) | 391 | 400 | 410 | 429 | |
| avian infectious bronchitis pol 1ab | (244) | ASINGAVAKTFEELPNGFMGSKI FTTLAFFKEAAVRVVE | | | | |
| bovine coronavirus pol 1ab | (390) | IDCEQDLCDPKGWVPGNMIDGEACTTCCHVYETGDL LAQ | | | | |
| Human corona 229E pol 1ab | (336) | EEHVNRMDTLCFNVRNSVTDECRLAMTCAEMTSNVR RQV | | | | |
| Murine hepatitis pol 1ab | (388) | VDCCGDTCDRGWVAGNMNDGFP CPGCTKNYMPWELEAQ | | | | |
| Consensus | (391) | IDC GDLCD FKGWVPNNMMDGF CTTLG YESAVRLAQ | | | | |
| Section 12 | | | | | | |
| | (430) | 430 | 440 | 450 | 468 | |
| avian infectious bronchitis pol 1ab | (283) | NIPNAPRGTKGFEEVVGNAKG TQVVVRGMRNDLTLLDOKA | | | | |
| bovine coronavirus pol 1ab | (429) | SSGVLPVNFVLTHTKSAAGYGGFGCKDSE TLYGQTVVYFG | | | | |
| Human corona 229E pol 1ab | (375) | ASGVLDISTGWFDDYDDIEAE-----SK-PWFVRKA | | | | |
| Murine hepatitis pol 1ab | (427) | SSGVIREGGVLEETQSTD TN-----RESERKLYGHAVVPFG | | | | |
| Consensus | (430) | SSGVIPIGTVLFTVSADAFG KDSFKLYG VV KA | | | | |

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FIGURE 4A (contd.)

| Section 13 | | | | | | |
|-------------------------------------|-------|--|-----|-----|-----|-----|
| | (469) | 469 | 480 | 490 | 507 | |
| avian infectious bronchitis pol 1ab | (322) | DIPVEPEGWSAII LDGHL CYVFRSGDRFYAAPLSGNEALS | | | | |
| bovine coronavirus pol 1ab | (468) | GCYYWS-PARNIWIPIILKSSVKSYDGLVYTGTVGCKATV | | | | |
| Human corona 229E pol 1ab | (405) | EDIFGP-CWSALASALKQLKVTITGELVRFVKSTICNSAVA | | | | |
| Murine hepatitis pol 1ab | (462) | SAVYWS-PCPGMWLPVITWSSVRSYSCLTYTGTVGCKATV | | | | |
| Consensus | (469) | D VYWS PWSAIWIPIIL SSVKSYDGL YTGTVGNKAIV | | | | |
| Section 14 | | | | | | |
| | (508) | 508 | 520 | 530 | 546 | |
| avian infectious bronchitis pol 1ab | (361) | DVHCCERVVCLSDGMTPEINDGLILAAIYSSFSVSELVLT | | | | |
| bovine coronavirus pol 1ab | (506) | KETNLICKALYDDYVQHKCGNLHORELLGVSEVWHKQLL | | | | |
| Human corona 229E pol 1ab | (443) | VMGGTICQILASMPKFLNAFDMFVTATQTVFCAVETCT | | | | |
| Murine hepatitis pol 1ab | (500) | QETDAICRSLYMDYVQHKCGNLEQRAILGLDDVYHROL | | | | |
| Consensus | (508) | VT ICRSLYLDYVQHKCGNL QRAILGVSDVWHEQLT | | | | |
| Section 15 | | | | | | |
| | (547) | 547 | 560 | 570 | 585 | |
| avian infectious bronchitis pol 1ab | (400) | ALKKCEPFKFLGHKFVYAKDAAVSFTLAKAATIAADVLRIT | | | | |
| bovine coronavirus pol 1ab | (545) | INRGVYKPTLENTDYENMRRAKFSLETETVCADGIMBFL | | | | |
| Human corona 229E pol 1ab | (482) | TAGKAFDKVFDYVLLDNALVKLVTTIKIKGVRERGINVKV | | | | |
| Murine hepatitis pol 1ab | (539) | VNRGDYSLIDENVDLFVKRRAEFAK-FATCGDGLVPLL | | | | |
| Consensus | (547) | INRKAY LLENVDLFNARRA VS KLEAVCADGLVPLL | | | | |
| Section 16 | | | | | | |
| | (586) | 586 | 600 | 610 | 624 | |
| avian infectious bronchitis pol 1ab | (439) | FOSARVIAEDVWSEFTEKSFEFWKEAYGKVRNLEEFVKIT | | | | |
| bovine coronavirus pol 1ab | (584) | LDDLVPRAVYLAVERGOALCDYADKICHAVVSKSKELLDV | | | | |
| Human corona 229E pol 1ab | (521) | YATVVVGSTEEVKS-----RVERSTAVLTIANYSKL | | | | |
| Murine hepatitis pol 1ab | (577) | LDGLVPRSYYLIKSGOAFISMVNFSHEVTDMMCDMALL | | | | |
| Consensus | (586) | LDSLVVRAYYLIKSGQAFS VKISHAVVSIA EMSKL | | | | |
| Section 17 | | | | | | |
| | (625) | 625 | 630 | 640 | 650 | 663 |
| avian infectious bronchitis pol 1ab | (478) | YVCKAQMSIVILA AVLGEDIMHIVS---QVLYKLGVLFT | | | | |
| bovine coronavirus pol 1ab | (623) | SLDSLSAAIHYLNSKITVDLAQHFSDFGTSFVSKIVHFFK | | | | |
| Human corona 229E pol 1ab | (554) | FDEGYTVVVGDMAYFVSDGYERTMASPNSVLTAVYKPL | | | | |
| Murine hepatitis pol 1ab | (616) | FMHDKVATKYVKKVTGKLAVRFKALGVAVVRKLTENED | | | | |
| Consensus | (625) | FLD LSAVI YLAAVIGDLAFRLMA G SVVSKIVHFF | | | | |
| Section 18 | | | | | | |
| | (664) | 664 | 670 | 680 | 690 | 702 |
| avian infectious bronchitis pol 1ab | (514) | KVVD FCDKHWKGF CVOLKRAKLTVTETFCVLKGV AQHCF | | | | |
| bovine coronavirus pol 1ab | (662) | TFTTSTAIAFAVLEHVLHGAYLVVESDIYFVKNTIPRYA | | | | |
| Human corona 229E pol 1ab | (593) | FAFN NVMGTRPEKEPTTVTCENLESAYLEVNDKITTEEQ | | | | |
| Murine hepatitis pol 1ab | (655) | LAVDIAASAAGWLCYQLVNGLEAVANGVITFVQEMPELV | | | | |
| Consensus | (664) | AVDI ALAFKWLCFQLL G FIV EAVIEFV IPEF | | | | |

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FIGURE 4A (contd.)

| | | | | | | |
|-------------------------------------|-------|---|-------------------|--------------------|-----------------|------------|
| | | | | | | Section 19 |
| | (703) | 703 | 710 | 720 | 730 | 741 |
| avian infectious bronchitis pol 1ab | (553) | QLLLDAIHSLYKSEFKKCALGRTHGDLLEFWKGGVHKLVQD | | | | |
| bovine coronavirus pol 1ab | (701) | SAVAQAFRSVAKVVLDLSLRVTFIDGLSCFKIGRRRTICLS | | | | |
| Human corona 229E pol 1ab | (632) | LDYSIDVIDNEILVKPNISLCVPLYVRDYVDKWDDFCRQ | | | | |
| Murine hepatitis pol 1ab | (694) | KNEVDKEKATFKVLIDSMVSSTLSGLTVVKTAENRVCLIA | | | | |
| Consensus | (703) | VSDAFKSLFKVVKDSISVSII | GLS | FK | G | RICLA |
| | | | | | | Section 20 |
| | (742) | 742 | 750 | 760 | 770 | 780 |
| avian infectious bronchitis pol 1ab | (592) | GD----- | | | | |
| bovine coronavirus pol 1ab | (740) | GSKIYEVERGLLHSSQLPLDVYDLIMPSSQVQKAKQKPIY | | | | |
| Human corona 229E pol 1ab | (671) | YS----- | | | | |
| Murine hepatitis pol 1ab | (733) | GSKVYEVVQKSTISAYVMPVGCSEAICLVGEIEP----- | | | | |
| Consensus | (742) | GSKIYEV | L A | LPL | D T | |
| | | | | | | Section 21 |
| | (781) | 781 | 790 | 800 | | 819 |
| avian infectious bronchitis pol 1ab | (594) | -----EIWFDAIDSDVDVEDIGVVQEKSIDFEVCD | | | | |
| bovine coronavirus pol 1ab | (779) | LKSGSGDFSLADSVVEVVTTSLETPCGYSEPPKVVADKIGI | | | | |
| Human corona 229E pol 1ab | (673) | -----NESWFEDDYRAFTSVLDITDAAVKAAESKA | | | | |
| Murine hepatitis pol 1ab | (766) | -----AVFEDDVVDVVKAPLLYQGCCCKPPTSFEKIGI | | | | |
| Consensus | (781) | | EDWVVDVVS | A LT | LGISDPPSTADKICI | |
| | | | | | | Section 22 |
| | (820) | 820 | 830 | 840 | | 858 |
| avian infectious bronchitis pol 1ab | (623) | DVTLPENQPGHMVQIEDDGKNYMEFFREKKDENIYYTPMS | | | | |
| bovine coronavirus pol 1ab | (818) | VDNVYMAKAGDKYYPVVVDG-HVGLLDQAWRVPCAGRRV | | | | |
| Human corona 229E pol 1ab | (703) | FVDTIVPPQPSILKVIDGGKIWNGVTKNVNSVRDWLKS | | | | |
| Murine hepatitis pol 1ab | (798) | VDKLYMAKCGDQFQPVVVDNDTVGVLDQCWRFPACAGKRV | | | | |
| Consensus | (820) | VV | LYMAKCGDIVYPVVVGK | WVGVL | DQ WRVPCAGKKV | |
| | | | | | | Section 23 |
| | (859) | 859 | 870 | 880 | | 897 |
| avian infectious bronchitis pol 1ab | (662) | QLGAINVVCKAGGKTVTFGETTVQELIPPPDVVPIKVSIE | | | | |
| bovine coronavirus pol 1ab | (856) | TFKEQPTVNETASTPKTIKVFYELDKDENTTLNTACGVF | | | | |
| Human corona 229E pol 1ab | (742) | KLNLTQQGLLGTCAKRFKRWLGITLLEAYNAFLDTVVSTV | | | | |
| Murine hepatitis pol 1ab | (837) | EFNDKPKVRKTFST-RKIKITFALDATFDSVLSKACSEE | | | | |
| Consensus | (859) | LND P V | KIAST RTIKITFILD | ENSVL | TAVSIF | |
| | | | | | | Section 24 |
| | (898) | 898 | 910 | 920 | | 936 |
| avian infectious bronchitis pol 1ab | (701) | CCGEPWN-----TTFKKAYKEPIEVDTLTVEQLLSV | | | | |
| bovine coronavirus pol 1ab | (895) | EVDDTVDMEEFYAVVIDAIEEKTSPCKELEGVCAKVS | | | | |
| Human corona 229E pol 1ab | (781) | KTGG-----LTFKTYAFDKPYIVTRDIVCKV | | | | |
| Murine hepatitis pol 1ab | (875) | EVDKDYTLDELDDVLDVLDVESTLSCKEHDVIGTKVCAI | | | | |
| Consensus | (898) | EVGD V LDE | VVIDAIE | TLSPCKEHDVIGDKVCAV | | |

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FIGURE 4A (contd.)

| Section 25 | | | | | | |
|-------------------------------------|--------|-------------|-----------------|------------------|-------------|-----------------------|
| | (937) | 937 | 950 | 960 | 975 | |
| avian infectious bronchitis pol 1ab | (733) | IYEKMCDDLK | FPEAPEPPPFEN | VALVDKNGRLLDQIKS | | |
| bovine coronavirus pol 1ab | (934) | LQKLEDNSLEF | DEAGFEVLASKLYCA | FTAPELDDDFLEE | | |
| Human corona 229E pol 1ab | (807) | ENKTEAEWLEF | PHNDRIKSFSTFES | AYMPIADPTHTDI | | |
| Murine hepatitis pol 1ab | (914) | LDRLAGDYVYL | DEGGDEVIAPRMYC | SFSAPDDEDCVAA | | |
| Consensus | (937) | LNKLEADWLF | LFPEAGEEVI | FSKLYCAFSAPD | DDDDCIDA | |
| Section 26 | | | | | | |
| | (976) | 976 | 990 | 1000 | 1014 | |
| avian infectious bronchitis pol 1ab | (772) | CHLIYRDYESD | DDIEEDAEECDT | DSGEAEFCDTN | ---- | |
| bovine coronavirus pol 1ab | (973) | SGVEEDDVEGE | ETDLTVTSAGE | PCVASEQEE | ----- | |
| Human corona 229E pol 1ab | (846) | EEVELLDAAEF | VEPGCGGITAVI | DEHVFYKKDG | VYYP--- | |
| Murine hepatitis pol 1ab | (953) | DVVDADENQDD | DAEDSAVLVADT | QEEEDGVAKQ | VEADSE | |
| Consensus | (976) | DVE | DD | EDD | DDSAILAADD | |
| | | DA | E | EEG | | |
| Section 27 | | | | | | |
| | (1015) | 1015 | 1020 | 1030 | 1040 | 1053 |
| avian infectious bronchitis pol 1ab | (807) | ----- | SECEE | DEDTKVLAL | IQDPASIKYPL | PLLED |
| bovine coronavirus pol 1ab | (1004) | ----- | SSEILED | TLDGPCVET | SDSOVEED | VEMSDFADLE |
| Human corona 229E pol 1ab | (882) | ----- | SNGTNILP | VAFKAAAGK | VSFSDD | VEVKDIEPVY |
| Murine hepatitis pol 1ab | (992) | ICVAHTGSQ | EELAE | PDVAGSQT | PIASABETE | VGAEASDRE |
| Consensus | (1015) | S | SEDL | EDD | AA | A IQ AEDVEV D ADLE |
| Section 28 | | | | | | |
| | (1054) | 1054 | 1060 | 1070 | 1080 | 1092 |
| avian infectious bronchitis pol 1ab | (838) | YSVYNGCIV | HKDAIDMVN | LPSG | ----- | ----- |
| bovine coronavirus pol 1ab | (1039) | SVIQDYENVC | FEFYTTE | ----- | ----- | ----- |
| Human corona 229E pol 1ab | (916) | RVKLCFEFE | DEKLVDC | EKATG | ----- | ----- |
| Murine hepatitis pol 1ab | (1031) | GIAEAKATV | CADA | VDACE | DOVEAFEIE | KVEDSILDELQT |
| Consensus | (1054) | VI | FE | VC | DAVDVCP | IG |
| Section 29 | | | | | | |
| | (1093) | 1093 | 1100 | 1110 | 1120 | 1131 |
| avian infectious bronchitis pol 1ab | (860) | ----- | ----- | ----- | ----- | EE |
| bovine coronavirus pol 1ab | (1057) | ----- | ----- | ----- | ----- | EFVKV |
| Human corona 229E pol 1ab | (938) | ----- | ----- | ----- | ----- | KKIK |
| Murine hepatitis pol 1ab | (1070) | ELNAPADKTY | EDVLAFDAVC | SEALS | SAFYAVPS | DETHFKV |
| Consensus | (1093) | | | | | KV |
| Section 30 | | | | | | |
| | (1132) | 1132 | 1140 | 1150 | 1160 | 1170 |
| avian infectious bronchitis pol 1ab | (862) | TFVVN | ----- | ----- | NCFEGAVKPL | PQKVVDV |
| bovine coronavirus pol 1ab | (1062) | LDLYVPKATR | NNCWLRSV | LAVMOKLE | CQFKDKNLQ | DEWV |
| Human corona 229E pol 1ab | (942) | HEG | ----- | DWDSFCKTI | QSALS | VVSCYVNLPTYI |
| Murine hepatitis pol 1ab | (1109) | CGFYSPAIE | RTNCWLRS | TLLIMOSL | PLEFKDL | EMOKLWL |
| Consensus | (1132) | DLY | P | R | NCWLRS | L VMQALPL FKDLNLQ LWV |

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FIGURE 4A (contd.)

| Section 31 | | | | | |
|--|--------|------------------|----------------|---------------|--------------|
| | (1171) | 1171 | 1180 | 1190 | 1209 |
| avian infectious bronchitis pol 1ab (884) | | EGDWGEAVDAQEQ | LCQQEEL | IQHTFFEEP | PVENSTGSSKTM |
| bovine coronavirus pol 1ab (1101) | | LYKQOYSOLFVDTLVN | KTLANTIVVP | QGGYVADFA | FWFLT |
| Human corona 229E pol 1ab (972) | | YDEEGGNDLSLPVMI | SEWLSVQQAQ | QEATLPDIAE | DDVV |
| Murine hepatitis pol 1ab (1148) | | SYKAGYDOCFVDKLV | SKSVKSTIIL | POGGYVADFA | FFELIS |
| Consensus (1171) | | LYK GYAQLFVD LVN | IPLSIILP | QGGYVADFA | FFFLT |
| Section 32 | | | | | |
| | (1210) | 1210 | 1220 | 1230 | 1248 |
| avian infectious bronchitis pol 1ab (923) | | EQVVVEDQELPVVEQ | IQDVVVYTPTD | LEVAKETAEE | VDE |
| bovine coronavirus pol 1ab (1140) | | LCDWQCVAYWKCIKC | IALKCLKGLD | AMFFYGDV | VSHVCK |
| Human corona 229E pol 1ab (1011) | | DQVEEVNSIETDIETV | VKHDVSPFEMP | FEELNGLKIL | KQ |
| Murine hepatitis pol 1ab (1187) | | QCSFKAYANWRCLFC | DMELKLOGLD | AMFFYGDV | SHMCK |
| Consensus (1210) | | DQVF A WKCIECDL | DLKL GLDAMFF | YGDV | VSHVCK |
| Section 33 | | | | | |
| | (1249) | 1249 | 1260 | 1270 | 1287 |
| avian infectious bronchitis pol 1ab (962) | | FILIFAMPKEEVVSQ | KDGAQIKOEPI | QVMKPORE-KK-- | |
| bovine coronavirus pol 1ab (1179) | | CGESMVLIDVDVPET | AHFALKKLLCA | FITKRSVYKA | AC |
| Human corona 229E pol 1ab (1050) | | LDNNCWVNSVMLQIQ | LGTGILDGDY | AMQFFKMG----- | |
| Murine hepatitis pol 1ab (1226) | | CGNSMTLLSADIETV | LHFQVRDDKF | CAFYTERKVF | RAAC |
| Consensus (1249) | | CGNSM LISVDVPET | LHGALKDD FCQF | VTPRKVFKA | AC |
| Section 34 | | | | | |
| | (1288) | 1288 | 1300 | 1310 | 1326 |
| avian infectious bronchitis pol 1ab (998) | | ----- | ----- | ----- | AK |
| bovine coronavirus pol 1ab (1218) | | VVDVNDSHSNAVVDG | KQIDDHRYTS | ITS DKFDFI | IGHGM |
| Human corona 229E pol 1ab (1082) | | ----- | ----- | ----- | ----- |
| Murine hepatitis pol 1ab (1265) | | AVDVNDCHSMAVVEG | KQIDGKVVTK | FIGDKFEDM | VGYGM |
| Consensus (1288) | | VDVND HSMNAVVDG | KQID VT DKFDFI | IGHGM | |
| Section 35 | | | | | |
| | (1327) | 1327 | 1340 | 1350 | 1365 |
| avian infectious bronchitis pol 1ab (1000) | | KFKVKPATCEKPKFL | EYKTCVGDLTV | VIAKATDEFKE | FC |
| bovine coronavirus pol 1ab (1257) | | SFSMTTFEIAQLYGS | CITENVCVKGDI | LKVSKRVKAE | V |
| Human corona 229E pol 1ab (1082) | | ----- | RVAKMIERCYTAE | QCIRGAMGDVG | LCMYRLIK |
| Murine hepatitis pol 1ab (1304) | | TFSMSPFELAQLYGS | CITPNVCFVKGDI | VIRVRLVNAE | V |
| Consensus (1327) | | SFSMSPFEIAQLYGS | CYTPNVCFVKGDI | LKVLKLVKA | EV |
| Section 36 | | | | | |
| | (1366) | 1366 | 1380 | 1390 | 1404 |
| avian infectious bronchitis pol 1ab (1039) | | LVNAANEHMTHGSG | VAKATADFCGLD | FVEYCEDYV | KKHL |
| bovine coronavirus pol 1ab (1296) | | VVNPAANGHMAHGG | VAKATAVAAGQ | OFVKETTTDM | VKSQ |
| Human corona 229E pol 1ab (1114) | | DLHTGFMVVDYKCS | CTSGRLEESCA | VLECTPTKKA | APPY |
| Murine hepatitis pol 1ab (1343) | | IVNPAANGHMAHGA | GVAGATAEKAG | SATIKETSDM | VKAQ |
| Consensus (1366) | | IVNPAANGHMAHGA | GVAKAIAE AGA | FVKETTTDM | VKAHG |

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FIGURE 4A (contd.)

| Section 37 | | | | | | |
|--|--------|--|------------|------------------------------|------------------------|-----------|
| | (1405) | 1405 | 1410 | 1420 | 1430 | 1443 |
| avian infectious bronchitis pol 1ab (1078) | | PQOR | ----- | ----- | ----- | ----- |
| bovine coronavirus pol 1ab (1335) | | VCATGDCYVSTGGKLGKTVLNIVGPDARTQGGKOSYALLE | | | | |
| Human corona 229E pol 1ab (1153) | | TCLNCNAPRMCTIROLOQTIIIFVQOKPEP | ----- | ----- | ----- | VNP |
| Murine hepatitis pol 1ab (1382) | | VCQVGECEYESAGGKLGCKVLNIVGPDARGHGKOCYSTIE | | | | |
| Consensus (1405) | | VCQ | GDCY S | GGKLGCK | VLNIVGPDAR | GKQ YALLE |
| Section 38 | | | | | | |
| | (1444) | 1444 | 1450 | 1460 | 1470 | 1482 |
| avian infectious bronchitis pol 1ab (1082) | | ----- | ----- | LVTPSFVKELQCVNNVVGPRHGDNNLHE | | |
| bovine coronavirus pol 1ab (1374) | | RVLKHLNKYDCVVTTLISAGIFSVPSDVSLLTYLLGTAEK | | | | |
| Human corona 229E pol 1ab (1185) | | VSEFVVKPVQSSIFRGAVSCCHYQTNIIYSQNLCDVGFGVN | | | | |
| Murine hepatitis pol 1ab (1421) | | RAYOHINKCDNVVTTLISAGIFSVPTDVSLLTYLLGVYTK | | | | |
| Consensus (1444) | | RAY | HINKCD | VVTTLISAGIFSVPSDVSLLTYLLG | L | K |
| Section 39 | | | | | | |
| | (1483) | 1483 | 1490 | 1500 | 1510 | 1521 |
| avian infectious bronchitis pol 1ab (1110) | | KIVAAYKIVLVDGVVNYVVPVLSLGIFGVDFKMSIDAMR | | | | |
| bovine coronavirus pol 1ab (1413) | | QVVLVSNNODEDELLSKCOITAVEGTRKLAERLSFNVGR | | | | |
| Human corona 229E pol 1ab (1224) | | KIQPWITN | ----- | DALNTTICKDADYNKMETSVTPIK | | |
| Murine hepatitis pol 1ab (1460) | | NVVLVSNNODDFDVIKCOVTSVACTKALSLOIAKNLGR | | | | |
| Consensus (1483) | | KVVLVSNNQDDFDVIAKQITLVDGTRKALALKLSINLIR | | | | |
| Section 40 | | | | | | |
| | (1522) | 1522 | 1530 | 1540 | 1550 | 1560 |
| avian infectious bronchitis pol 1ab (1149) | | EAPEGCTIRVLLES | ----- | ----- | ----- | ----- |
| bovine coronavirus pol 1ab (1452) | | SLVYETDANKLLLSNDVAEVSTFNVLDVLSLRHDIALD | | | | |
| Human corona 229E pol 1ab (1256) | | NTVDTTTPKEEFVVKERLNAFLVHDNVAFYQGDVDTVNG | | | | |
| Murine hepatitis pol 1ab (1499) | | DNKFEVINACSSLES | ----- | ESCEVSSSYDVLQEVFAIRHDIOLD | | |
| Consensus (1522) | | DIVF T A | LLFS DL | EVSSHDLVDV | ALRHD I LD | |
| Section 41 | | | | | | |
| | (1561) | 1561 | 1570 | 1580 | 1590 | 1599 |
| avian infectious bronchitis pol 1ab (1163) | | ----- | ----- | ----- | ----- | ----- |
| bovine coronavirus pol 1ab (1491) | | DDARTFVQSNVDVVPPEGWRVVNKKFYQINGVRTIVKYFECF | | | | |
| Human corona 229E pol 1ab (1295) | | VDFFDFIVNAANENLAHGGGLAKALDVYTKGKLQRLSKEH | | | | |
| Murine hepatitis pol 1ab (1537) | | DDARFVQANMDCTPTDNRVLVNKEDSVDGVRTIKYFECF | | | | |
| Consensus (1561) | | DDAR | FVQANMD LP | GWRLVNKFD I | GVRTIKYFECF | |
| Section 42 | | | | | | |
| | (1600) | 1600 | 1610 | 1620 | 1638 | |
| avian infectious bronchitis pol 1ab (1163) | | --LSQEHID | ----- | ----- | YFD--VTCKOKTLY | |
| bovine coronavirus pol 1ab (1530) | | GGIDTICSQDKVFGYVQOGSEFNKATVAQIKALFEDKVDIL | | | | |
| Human corona 229E pol 1ab (1334) | | IGLAG | ----- | ----- | KVKVGTGVMVECDLSLRIFNVV | |
| Murine hepatitis pol 1ab (1576) | | GGIFVSSQGNKEGYVQNGSEKESVSQIRALLANKVDVH | | | | |
| Consensus (1600) | | GGIAI | SQDK | FGYVQNGSEK | ATVAQIKALS | SLKKVDIL |

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FIGURE 4A (contd.)**Section 43**

| | (1639) | 1639 | 1650 | 1660 | 1677 |
|--|--------|-------|--------|--------|--------------------------|
| avian infectious bronchitis pol 1ab (1182) | LT | EDGVK | YRSIVL | KPGDSL | LGQFG-----QVYAKN |
| bovine coronavirus pol 1ab (1569) | LT | VDGVN | ETNR | FMPV | GESFGKSLGNVECDGVNVTKHKCD |
| Human corona 229E pol 1ab (1360) | GER | KKEH | ERD | LLKAY | NTINNEQGTPLTPILSCGIFGIK |
| Murine hepatitis pol 1ab (1615) | CT | VDGVN | FNSCC | VAEGE | VFCKTLG |
| Consensus (1639) | LT | VDGVN | FNSIL | VK GES | FGKSLG |

Section 44

| | (1678) | 1678 | 1690 | 1700 | 1716 |
|--|--------|--------|-------|-------|------------|
| avian infectious bronchitis pol 1ab (1211) | K | IVFTAD | DVEDK | ETLYV | PTTDKSILEY |
| bovine coronavirus pol 1ab (1608) | I | NYKGR | VFFQ | FDNLS | SEDIKAV |
| Human corona 229E pol 1ab (1399) | L | ETSLE | VL | LDVC | NTKEVK |
| Murine hepatitis pol 1ab (1654) | A | IKKGR | VFFQ | MSLS | ADLVA |
| Consensus (1678) | I | IKKGR | VFFQ | MSLS | ADLVA |

Section 45

| | (1717) | 1717 | 1730 | 1740 | 1755 |
|--|--------|------|------|------|------|
| avian infectious bronchitis pol 1ab (1250) | O | T | L | A | K |
| bovine coronavirus pol 1ab (1647) | L | V | N | C | S |
| Human corona 229E pol 1ab (1438) | V | Q | K | E | P |
| Murine hepatitis pol 1ab (1693) | L | G | - | M | C |
| Consensus (1717) | L | M | K | N | V |

Section 46

| | (1756) | 1756 | 1770 | 1780 | 1794 |
|--|--------|------|------|------|------|
| avian infectious bronchitis pol 1ab (1289) | R | E | K | G | E |
| bovine coronavirus pol 1ab (1686) | K | F | K | I | V |
| Human corona 229E pol 1ab (1476) | C | V | A | D | D |
| Murine hepatitis pol 1ab (1731) | K | E | P | K | W |
| Consensus (1756) | K | F | K | I | V |

Section 47

| | (1795) | 1795 | 1800 | 1810 | 1820 | 1833 |
|--|--------|------|------|------|------|------|
| avian infectious bronchitis pol 1ab (1327) | A | N | W | L | I | A |
| bovine coronavirus pol 1ab (1725) | S | R | D | E | L | R |
| Human corona 229E pol 1ab (1515) | V | D | I | N | K | |
| Murine hepatitis pol 1ab (1770) | I | D | E | M | B | |
| Consensus (1795) | I | D | F | L | R | |

Section 48

| | (1834) | 1834 | 1840 | 1850 | 1860 | 1872 |
|--|--------|------|------|------|------|------|
| avian infectious bronchitis pol 1ab (1360) | -- | YEL | R | G | -- | -- |
| bovine coronavirus pol 1ab (1764) | M | H | F | G | T | |
| Human corona 229E pol 1ab (1551) | N | N | V | Q | R | |
| Murine hepatitis pol 1ab (1809) | M | H | F | G | T | |
| Consensus (1834) | M | H | F | G | T | |

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FIGURE 4A (contd.)

| Section 49 | | | | | | |
|--|--------|-------|------|--------|--------|-------|
| | (1873) | 1873 | 1880 | 1890 | 1900 | 1911 |
| avian infectious bronchitis pol 1ab (1393) | | NNTDE | VI | EASLPY | LLFATD | GPA |
| bovine coronavirus pol 1ab (1803) | | SNTPE | AS | VRLEK | GVGSAN | TFKGD |
| Human corona 229E pol 1ab (1590) | | SFVGG | LL | KAAEAK | VITIK | VTEDG |
| Murine hepatitis pol 1ab (1848) | | SNTPE | GR | KLPDD | VVAAN | IFTGG |
| Consensus (1873) | | SNTPE | LR | KLP | VISAN | ITDGG |
| Section 50 | | | | | | |
| | (1912) | 1912 | 1920 | 1930 | 1940 | 1950 |
| avian infectious bronchitis pol 1ab (1432) | | STNSG | H | CYTQ | AAQAF | DN |
| bovine coronavirus pol 1ab (1842) | | DA | SNV | K | VTDVT | NLS |
| Human corona 229E pol 1ab (1629) | | VG | VIAD | K | DKDLS | AMP |
| Murine hepatitis pol 1ab (1887) | | DA | CNVN | K | VSEAK | NFTD |
| Consensus (1912) | | DA | NV | K | VTDAS | GNL |
| Section 51 | | | | | | |
| | (1951) | 1951 | 1960 | 1970 | 1989 | |
| avian infectious bronchitis pol 1ab (1471) | | AFKNE | T | SLP | AKQ | S |
| bovine coronavirus pol 1ab (1881) | | VKKTE | Y | N | P | D |
| Human corona 229E pol 1ab (1668) | | KDA | V | T | F | A |
| Murine hepatitis pol 1ab (1926) | | VKC | V | E | K | P |
| Consensus (1951) | | VKK | V | E | Y | A |
| Section 52 | | | | | | |
| | (1990) | 1990 | 2000 | 2010 | 2028 | |
| avian infectious bronchitis pol 1ab (1510) | | TDFEQ | W | Y | D | S |
| bovine coronavirus pol 1ab (1920) | | YTNF | K | L | I | G |
| Human corona 229E pol 1ab (1707) | | CIALQ | Y | S | K | P |
| Murine hepatitis pol 1ab (1965) | | YTNF | K | L | V | G |
| Consensus (1990) | | YTNF | Q | L | I | G |
| Section 53 | | | | | | |
| | (2029) | 2029 | 2040 | 2050 | 2067 | |
| avian infectious bronchitis pol 1ab (1549) | | LTLK | V | R | G | I |
| bovine coronavirus pol 1ab (1959) | | GDV | V | L | A | T |
| Human corona 229E pol 1ab (1746) | | RLM | K | G | D | K |
| Murine hepatitis pol 1ab (2004) | | GDV | V | L | A | S |
| Consensus (2029) | | GDV | V | L | A | S |
| Section 54 | | | | | | |
| | (2068) | 2068 | 2080 | 2090 | 2106 | |
| avian infectious bronchitis pol 1ab (1588) | | VLD | A | I | S | L |
| bovine coronavirus pol 1ab (1998) | | TYFN | R | P | L | V |
| Human corona 229E pol 1ab (1785) | | AKF | K | N | S | V |
| Murine hepatitis pol 1ab (2043) | | TYFN | R | P | S | V |
| Consensus (2068) | | TYFN | R | S | L | L |

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FIGURE 4A (contd.)

| Section 55 | | | | | |
|--|---|---------------------------|-----------------|-----------------|-----------|
| | (2107) 2107 | 2120 | 2130 | 2145 | |
| avian infectious bronchitis pol 1ab (1615) | ----- | ----- | ----- | -----KSLHT | |
| bovine coronavirus pol 1ab (2024) | ----- | ----- | ----- | -----DISESDAKES | |
| Human corona 229E pol 1ab (1812) | ----- | ----- | ----- | -----YCVHG | |
| Murine hepatitis pol 1ab (2082) | PGADASAGAGIAKEQKACASASVEDQVVTEVRQEPSVSA | | | | |
| Consensus (2107) | | | DI | SVHA | |
| Section 56 | | | | | |
| | (2146) 2146 | 2160 | 2170 | 2184 | |
| avian infectious bronchitis pol 1ab (1620) | PTFWENAENFVRMGDKIGCVTMGLWRAEHLNKPNIERIF | | | | |
| bovine coronavirus pol 1ab (2034) | KEINITKLSGVKKPFKVEDSVIVNDDTSEIKYVKSLSTIV | | | | |
| Human corona 229E pol 1ab (1817) | --LKYYSRVRSVRGRALIVSVEQLEFCAQSRLISGVAYT | | | | |
| Murine hepatitis pol 1ab (2121) | ADVKEVKLNGVKKPKVKEGSSVVNDPTSETKVVKSLSTIV | | | | |
| Consensus (2146) | DIKEIKLNGVKKP | KIEG | SVIVNDPTSE | SKLVKSLSTIV | |
| Section 57 | | | | | |
| | (2185) 2185 | 2190 | 2200 | 2210 | 2223 |
| avian infectious bronchitis pol 1ab (1659) | NTAKKALVSSVTTQCGKLDIGKAATFIADKVGGGVVRN | | | | |
| bovine coronavirus pol 1ab (2073) | DVYDMWLTGCRYVVRTANALSMANNVETTRKFTKFGMTL | | | | |
| Human corona 229E pol 1ab (1854) | AFSGPVDKCHYTYDTAKKSMYDGDREVKHDLSSLSTIS | | | | |
| Murine hepatitis pol 1ab (2160) | DVYDMFLTCKKYVWTANELSRLVNSRTVREYVKWCKGK | | | | |
| Consensus (2185) | DVYDMELTCKKYVV | TANKLS | VNSPTIRKVIKFGVT | | |
| Section 58 | | | | | |
| | (2224) 2224 | 2230 | 2240 | 2250 | 2262 |
| avian infectious bronchitis pol 1ab (1698) | ITDSIKGLICGITRG----- | | | | -----HFER |
| bovine coronavirus pol 1ab (2112) | VSIPIDDLNLRERKPVENVVKAVRNKISACENFTKWLFLV | | | | |
| Human corona 229E pol 1ab (1893) | VVMVGGYVAPVNTVKPKPVINQIDDKAQKFFDFGDFLIH | | | | |
| Murine hepatitis pol 1ab (2199) | IVTPAKLILLRDERQETVAPKVVKAKALACYCAVKNFLL | | | | |
| Consensus (2224) | IVIPIKLL | LRD K | F VIK VK KA | ACF | FIKWLIL |
| Section 59 | | | | | |
| | (2263) 2263 | 2270 | 2280 | 2290 | 2301 |
| avian infectious bronchitis pol 1ab (1716) | KMSPOFLKTLMFELFYFLKAS----- | | | | -----V |
| bovine coronavirus pol 1ab (2151) | LLFGWIKRISADNKVIYTTTEVASKLTCKLVALAFKNALLT | | | | |
| Human corona 229E pol 1ab (1932) | NFVIEFTWLLSMFTLCKTAVTTGDVKIMAKAPORTGVVL | | | | |
| Murine hepatitis pol 1ab (2238) | YCESWIKENTDNKVIYTTTEVASKLTCKLCCLAEKNALQT | | | | |
| Consensus (2263) | LF WIKFSLDNKVIYTTTEVASKLT | KL | LAFKNALLT | | |
| Section 60 | | | | | |
| | (2302) 2302 | 2310 | 2320 | 2330 | 2340 |
| avian infectious bronchitis pol 1ab (1741) | VASYKTVLCKVVLATLLIV | EVYTSNPEVMFTGIRVLDPL | | | |
| bovine coronavirus pol 1ab (2190) | FKWSVVARGACIIATIFELL | FNFIYANVILSDFYLPKIG | | | |
| Human corona 229E pol 1ab (1971) | KRSLKYNLKASAAVLKSKWLLAKETKLLLLINTLYSVV | | | | |
| Murine hepatitis pol 1ab (2277) | FNWSVVSRRGEFLVATVELL | FNFIYANVILSDFYLPNTG | | | |
| Consensus (2302) | FKWSVVARGA | IIATIFLLWENFIYANVILSDFYLP | IG | | |

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FIGURE 4A (contd.)

| Section 61 | | | | |
|--|---|------------------------------------|--------------------|--------------------------|
| | (2341) 2341 | 2350 | 2360 | 2379 |
| avian infectious bronchitis pol 1ab (1780) | FEGLSC | PPYKDYG | ----- | KDSFDVLRYS |
| bovine coronavirus pol 1ab (2229) | FLPTFVCKTAQWIKSTESLVTICDLYSIQDVGFKNQYCN | | | |
| Human corona 229E pol 1ab (2010) | LLCVRF | ---PEN--- | ECSETVN--- | GYAKSNFVKDDYD |
| Murine hepatitis pol 1ab (2316) | FLPTFV | QIVAMFKTTEGGVSTICDFYQVTDLGYRISSEFN | | |
| Consensus (2341) | FLPTFVG | I W KSTF L TICD Y IKDLGFK | | YCN |
| Section 62 | | | | |
| | (2380) 2380 | 2390 | 2400 | 2418 |
| avian infectious bronchitis pol 1ab (1804) | DDFI RV | LHDKDS | HLNKHAYS | EQVYKDAASGFIENW |
| bovine coronavirus pol 1ab (2268) | GSIACQELAGEDMDNYKALDV | OYEADRRAFVDYTG | | |
| Human corona 229E pol 1ab (2041) | GSLG | KMLFGYQELSQFSHDDV | WKHTTDFLFSNMQPF | |
| Murine hepatitis pol 1ab (2355) | GSMV | ELQFSGFDM | DNYDATNV | QHVDRRLSFDYISL |
| Consensus (2380) | GSIICKLCLAGFDM | LDNYKHIDVVQHVDRRLS | DY V | |
| Section 63 | | | | |
| | (2419) 2419 | 2430 | 2440 | 2457 |
| avian infectious bronchitis pol 1ab (1843) | NWLYLVEFLLEFVKPVAG | ----- | FVI-- | ICYCVKYLVLN |
| bovine coronavirus pol 1ab (2307) | LKTVIELIVSYALYTAWFXPLFALISIQILTTWLPELFM | | | |
| Human corona 229E pol 1ab (2080) | LVMVLLIFG | ----- | DNYERCFLLYEVAOMIS | |
| Murine hepatitis pol 1ab (2394) | EKLVELVLCYSLYTVCFYPLFVLIGMOLLTTWLPELFM | | | |
| Consensus (2419) | IKLVLELIIGYALYTA | FYPLF | LIHQILTTWLPELFM | |
| Section 64 | | | | |
| | (2458) 2458 | 2470 | 2480 | 2496 |
| avian infectious bronchitis pol 1ab (1874) | STVLQTCVCTLDWEVOTVFSHFNFMGAGFYFWLFYKLYT | | | |
| bovine coronavirus pol 1ab (2346) | LSTLHWSVRLLVSLANMLPAHVFMREYILTASFILFII | | | |
| Human corona 229E pol 1ab (2107) | TVGVFLGYKETNWEHLHFIFFDVICDELLVTVIVIKVVISF | | | |
| Murine hepatitis pol 1ab (2433) | LETMIHSARLEFVEVANMLPAFTLLRFYIVVTAMYKVYCL | | | |
| Consensus (2458) | LSTLHWSVRLLVWFANMLPAHVILRFYIVI | ALIKVI | L | |
| Section 65 | | | | |
| | (2497) 2497 | 2510 | 2520 | 2535 |
| avian infectious bronchitis pol 1ab (1913) | QV | HLIYCKDVT | EV | KRVARSNQEVSVVGGGRKQIVH |
| bovine coronavirus pol 1ab (2385) | FRHVAYG | SKPG | LF | CYKRNRSLSVKCSTIGGMIRYYD |
| Human corona 229E pol 1ab (2146) | VRHVLEGG | ENBD | IA | SKSARLKEFPVNTIINGVQORSEY |
| Murine hepatitis pol 1ab (2472) | CRHVMYGC | SKPG | LF | CYKRNRSVVKCSTVGGSLRYD |
| Consensus (2497) | RHVIYGC | SKPGCLFCYKRNRS | LRVKVSTIVGGMIRYYD | |
| Section 66 | | | | |
| | (2536) 2536 | 2550 | 2560 | 2574 |
| avian infectious bronchitis pol 1ab (1952) | MYTNSGYNECKRENWYCRNCDYGHQNFMSPEVAGETS | | | |
| bovine coronavirus pol 1ab (2424) | VMANGGTGFCCKKHQWNCINCD | SYKPGNTFITVEAALDLS | | |
| Human corona 229E pol 1ab (2185) | VMANG | GSKCKKHREFEVD | DSYGYGSI | ITPEVSRREIG |
| Murine hepatitis pol 1ab (2511) | VMANG | GTGELTKKHQWNCIN | NSWKPGNTFITHEAADLS | |
| Consensus (2536) | VMANGGTGFCCKKHQWNCIN | CD | SYKPGNTFITPEVAADLS | |

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FIGURE 4A (contd.)

| Section 67 | | | | | |
|--|--------|--------------|------------------|-------------------|----------------------------|
| | (2575) | 2575 | 2580 | 2590 | 2600 |
| avian infectious bronchitis pol 1ab (1991) | | EKT | RRHMKPTAYT | HHVVDEACLVDDFVN | KYKAATPGKD |
| bovine coronavirus pol 1ab (2463) | | KEL | RRPTQ | EDVA | HTVVDVKQVGCYMRIFYERDGGORTY |
| Human corona 229E pol 1ab (2224) | | NIT | TNVQ | GPA | VMIDKVEFENGGEYRLYSCETFWRYN |
| Murine hepatitis pol 1ab (2550) | | KEL | RPVNC | DS | YSVTEVKQVGC |
| Consensus (2575) | | KEL | RPVQPTD | AYHTVTEVKQVGC | CFMRLFYERDGGOR Y |
| Section 68 | | | | | |
| | (2614) | 2614 | 2620 | 2630 | 2640 |
| avian infectious bronchitis pol 1ab (2030) | | SASSAVKCF | SVTDFLKKAVFLKEAL | KCEQIS | ADGFIVCN |
| bovine coronavirus pol 1ab (2502) | | DDVNASL | FVDYSNLLH | SKVKGVP | NNHVVVVE |
| Human corona 229E pol 1ab (2263) | | FDITESKY | SCKEVFKN | --- | CNVLD |
| Murine hepatitis pol 1ab (2589) | | DDVNASL | FVDMNGLLH | SKVKGVP | ETHVVVVE |
| Consensus (2614) | | DDVNASL | FVDMS | LLH | SKVKGVPDLHVVVVEND |
| Section 69 | | | | | |
| | (2653) | 2653 | 2660 | 2670 | 2680 |
| avian infectious bronchitis pol 1ab (2069) | | TQSAHALEEAKN | AIYYA | YCKP | ELLILDQATYEQLVVE |
| bovine coronavirus pol 1ab (2535) | | ---- | ADKANFLN | AVFYA | QSFRLHLMVDKNLITTTANTG |
| Human corona 229E pol 1ab (2293) | | ---- | TNVTVQVKN | SVYFS | LICRIKLVQSE |
| Murine hepatitis pol 1ab (2622) | | ---- | ADKAGELG | AVEYA | QSYRPMMLMVEKKITTTANTG |
| Consensus (2653) | | ---- | ADKANFLN | AAVFYA | QSLCRPILMVDK LITTLNVG |
| Section 70 | | | | | |
| | (2692) | 2692 | 2700 | 2710 | 2720 |
| avian infectious bronchitis pol 1ab (2108) | | PVS | KSVIDKVC | SISS | LISVDTAATN |
| bovine coronavirus pol 1ab (2570) | | TSVTE | TMEDVYVD | TFLSMEDV | KKSNAL |
| Human corona 229E pol 1ab (2328) | | FNG | --- | VILHKA | IDVERN |
| Murine hepatitis pol 1ab (2657) | | LSVS | RTMEDLYVDS | LLNMLD | VERKSE |
| Consensus (2692) | | SVSK | TMEDLYVD | TLLSIFD | VDKKSLNA I AH.SIK |
| Section 71 | | | | | |
| | (2731) | 2731 | 2740 | 2750 | 2769 |
| avian infectious bronchitis pol 1ab (2134) | | ----- | YKAGTL | RDALLSIT | KDEEAVDMAIFCHN |
| bovine coronavirus pol 1ab (2609) | | GTOT | CKVLD | TFLSCARK | SCSIDSDVDTKCLADSVMSAVS |
| Human corona 229E pol 1ab (2352) | | ----- | MSLA | ECKRA | TGLSLSDHETSAISNAHR |
| Murine hepatitis pol 1ab (2696) | | GVOLE | QVMDTE | IGCARRK | CAIDSDVETKSTTKSVMSAVN |
| Consensus (2731) | | G QI | VLD | TFISCARKKCAIDSDVD | TKEITDSVMSAVN |
| Section 72 | | | | | |
| | (2770) | 2770 | 2780 | 2790 | 2808 |
| avian infectious bronchitis pol 1ab (2162) | | HDVDY | TGCGFTNV | TPSGID | TGKLT |
| bovine coronavirus pol 1ab (2648) | | AGLE | LTDE | SCN | LVPT |
| Human corona 229E pol 1ab (2380) | | CDVLL | SDLS | EN | FMSS |
| Murine hepatitis pol 1ab (2735) | | AGVD | FTDE | SCN | LVPT |
| Consensus (2770) | | AGVD | LTDE | SCN | LVPT |

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FIGURE 4A (contd.)

| Section 73 | | | | | | |
|--|--------|---------|------------|--------------|-------------------------|---------------------|
| | (2809) | 2809 | 2820 | 2830 | 2847 | |
| avian infectious bronchitis pol 1ab (2201) | | ANLP | KNAP-- | EVV | KFSELIKLEDSCLKYLISATVKS | |
| bovine coronavirus pol 1ab (2686) | | VOGN | AKIAGVSCIT | SVDAFNQI | SDFQHKLKACCKT | |
| Human corona 229E pol 1ab (2419) | | VNAN | LTKDOTPIV | HAKDFNSL | SAEGRKYLVKTSKAK | |
| Murine hepatitis pol 1ab (2773) | | VOAN | VAKAANVACI | SVDAFNQI | SADLOHRLRKACSKT | |
| Consensus (2809) | | VNAN | VAKAANVPCI | WSVDAFNQLSAD | QKYLRKAC KTG | |
| Section 74 | | | | | | |
| | (2848) | 2848 | 2860 | 2870 | 2886 | |
| avian infectious bronchitis pol 1ab (2238) | | VREFI | KSGAKQVI | ACHTQKLL | VEKKAGGIVSGTFKCFK | |
| bovine coronavirus pol 1ab (2725) | | LKCLKL | TYNKQ-- | MANVSVLT | TPPSLKGA | |
| Human corona 229E pol 1ab (2458) | | LTLL | INENQAV | TOIPATS | IVAKQGAGDAGH | |
| Murine hepatitis pol 1ab (2812) | | LRIKLT | TYNKQ-- | EANVPI | LTTPPSLKGA | |
| Consensus (2848) | | LKFKLT | TYNKQ | VANVPILT | TPPSLKAGAVFS | |
| Section 75 | | | | | | |
| | (2887) | 2887 | 2900 | 2910 | 2925 | |
| avian infectious bronchitis pol 1ab (2277) | | SYFKWLL | IFYILET | ACCSGY | YYYMEVSKSFVHPMYDVNST | |
| bovine coronavirus pol 1ab (2755) | | ----- | YFVYVCE | LLSLVCF | EGGLWCHMPTTYVHKSDFQI | |
| Human corona 229E pol 1ab (2490) | | ----- | SLTNLWLL | CGVGLI | QFMYLCFFMPYFMYDIVSS | |
| Murine hepatitis pol 1ab (2842) | | ----- | RMLQWTF | EVANLTC | FIVLWALMPTYAVHKSDMOL | |
| Consensus (2887) | | ----- | ILYILEFLA | LVCFI | LWLLMPTYHVMYS | |
| Section 76 | | | | | | |
| | (2926) | 2926 | 2940 | 2950 | 2964 | |
| avian infectious bronchitis pol 1ab (2316) | | LHVEGF | FLVIDKGV | LRVLPEDT | CFSHKVNEDAEWGRPY | |
| bovine coronavirus pol 1ab (2788) | | PVYAS | YVLDNVL | RDVSVEDV | FAFKFHOEDQWYESTF | |
| Human corona 229E pol 1ab (2523) | | FEGYDF | LYIENGOL | KNFEAPLK | VRVVFENFEDWHYARF | |
| Murine hepatitis pol 1ab (2875) | | PLYASF | FLVIDN | VLRDVS | VTDAEFAKFNQEDQWYESTF | |
| Consensus (2926) | | PLYASF | KVIDNGVLR | DVSVED | CFANKFENFDQWYESTF | |
| Section 77 | | | | | | |
| | (2965) | 2965 | 2970 | 2980 | 2990 | 3003 |
| avian infectious bronchitis pol 1ab (2355) | | DNSRNC | PIVTAVID | GDGTVA | TGVPGF | MSWVMDGVMFIHM |
| bovine coronavirus pol 1ab (2827) | | GLSYY | NSMA | ----- | CPIVVA | VVDQDLGSTVFNVP |
| Human corona 229E pol 1ab (2562) | | GFTPL | NK-Q | ----- | SCPIV | VGVSEIVNTVAGIPSNVYL |
| Murine hepatitis pol 1ab (2914) | | GLAYY | RNSKA | ----- | CPVVVA | VIDODIGHTLFNVPTTVLR |
| Consensus (2965) | | GLSYY | NSMA | ----- | CPIVVA | VGVQDIVSTVFNVP |
| Section 78 | | | | | | |
| | (3004) | 3004 | 3010 | 3020 | 3030 | 3042 |
| avian infectious bronchitis pol 1ab (2394) | | TQTERK | PWYIPT | WFNREI | VGYYQDS | ITTEGSEYTSIALF |
| bovine coronavirus pol 1ab (2862) | | YGYHVL | HFITHA | LSADGV | QCYPHS | QTSYSNIFYASGCVL |
| Human corona 229E pol 1ab (2594) | | VGKTL | IFETLQ | AAFGN | AGVCYD | IFGVTTPEK |
| Murine hepatitis pol 1ab (2949) | | YGFHVL | HFITHA | FATDSV | QCYPH | MOIPYDNEYASGCVL |
| Consensus (3004) | | YGFHVL | HFITHA | FANDGV | QCYPHS | QIPY NIFYASGCVL |

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FIGURE 4A (contd.)

| Section 79 | | | | | | |
|--|--------|------------------|--------------------|------------------|-------------|--------------|
| | (3043) | 3043 | 3050 | 3060 | 3070 | 3081 |
| avian infectious bronchitis pol 1ab (2433) | | SAR | LYLTASNT | POLYCFNGDNDAPGAL | PFG | TI PHRV |
| bovine coronavirus pol 1ab (2901) | | SSACTM | FAMADGSPQ | PYCYTEGLM | QNASLYS | SLVRHV |
| Human corona 229E pol 1ab (2627) | | ISA | TRLEGLG | GN-NVYC | YNTALMEG | SLPYSSIQANAY |
| Murine hepatitis pol 1ab (2988) | | SSL | TMLAHADGT | PHPYCMT | GGVMHNASLYS | LIAPHVR |
| Consensus (3043) | | SSACTMLAAADGSPNP | PYCYTDGLM | NASPYSS | LIIPHVR | |
| Section 80 | | | | | | |
| | (3082) | 3082 | 3090 | 3100 | 3110 | 3120 |
| avian infectious bronchitis pol 1ab (2472) | | FQPNG-- | VRLIVPQQILHTPYV | KFVSDSY | CRGSV | EYT |
| bovine coronavirus pol 1ab (2940) | | NLANAKG | FIREFPEVLR | REGLVRI | RTRSMSY | CRVGL |
| Human corona 229E pol 1ab (2665) | | KYDNGN | FIKLP | EVIAQGGFRT | RTIATK | CRVGE |
| Murine hepatitis pol 1ab (3027) | | NLAS | SNGVIRFPEV | VSEGI | VRV | RTRSM |
| Consensus (3082) | | NLANGNGVIRFPEV | L | EGIVRVVR | RTRSMSY | CRVGL |
| Section 81 | | | | | | |
| | (3121) | 3121 | 3130 | 3140 | 3159 | |
| avian infectious bronchitis pol 1ab (2509) | | RP | YCVSLNPQW | LFNDEYTSKPC | VEL | CRSTVRE |
| bovine coronavirus pol 1ab (2979) | | DE | ICFNEN | NGSW | LNN | DYRSLP |
| Human corona 229E pol 1ab (2704) | | NAGV | CEGEDKWE | NDG--- | RVANGYV | CTGLWN |
| Murine hepatitis pol 1ab (3066) | | DE | ICFNEN | RSW | LNN | PYRAMP |
| Consensus (3121) | | DEGICFNENKSWVL | NNDYRSLP | GTFCGR | VFDLIF | QIL |
| Section 82 | | | | | | |
| | (3160) | 3160 | 3170 | 3180 | 3198 | |
| avian infectious bronchitis pol 1ab (2548) | | STFFETG | MNPN-IYMQLATM | FLLLVVV | VF | FAMV |
| bovine coronavirus pol 1ab (3018) | | KGLAC | PVDELALTASSIAGAIL | AVIVVL | VF | YYLIK |
| Human corona 229E pol 1ab (2740) | | SMFSS | SFSVAAMSGQILLNCAL | GAFAL | FCC | FLV |
| Murine hepatitis pol 1ab (3105) | | GGLVR | PIDDEFALTASSVAGAIL | AVIVVL | VF | YYLIK |
| Consensus (3160) | | SGLASPVDF | ALTASSIAGAIL | AVIVVL | IFYYLIK | |
| Section 83 | | | | | | |
| | (3199) | 3199 | 3210 | 3220 | 3237 | |
| avian infectious bronchitis pol 1ab (2586) | | KAYAT | T | FTTMLVWVI | AFILC | HSYNSV |
| bovine coronavirus pol 1ab (3057) | | G | DYTS | IVFVNVIVWC | VFMMLF | FQVYPTL |
| Human corona 229E pol 1ab (2779) | | G | DL | SVGLCTVVVAVL | LNNMSYI | TQNLVT |
| Murine hepatitis pol 1ab (3144) | | G | DYTS | IVFVNVIVWC | IFLMLF | FQVYPTL |
| Consensus (3199) | | FGDYTSIVF | INVIW | CINFLMLF | VFVQVYPTL | SCIYAI |
| Section 84 | | | | | | |
| | (3238) | 3238 | 3250 | 3260 | 3276 | |
| avian infectious bronchitis pol 1ab (2625) | | CNASL | VTSRNTVIMHCWLV | FTFGLT | VT | WLACCL |
| bovine coronavirus pol 1ab (3096) | | F | YATLYFPSEISVIMH | LQWLVMYGT | IMPL | WLC |
| Human corona 229E pol 1ab (2818) | | F | ATRSR | L--YA-WI | WCAAYLIA | ISFAW |
| Murine hepatitis pol 1ab (3183) | | F | YTTLYFPSEISVIMH | LQWLVMYGT | IMPL | WLC |
| Consensus (3238) | | FYTTLYFPSEISVIMH | LQWLVMYGS | IMPL | WLC | IIYIAV |

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FIGURE 4A (contd.)

| Section 85 | | | | | | |
|--|--------|------------------------------|----------------------|------------------|--------------|-----------------|
| | (3277) | 3277 | 3290 | 3300 | 3315 | |
| avian infectious bronchitis pol 1ab (2664) | | LYMYTPLFLWCYGTTRKNTKRLYDGNFV | NYDLA | AKSL | | |
| bovine coronavirus pol 1ab (3135) | | VS----- | NHAFWVFAYCRR | LGTSVRSDGTFEEM | ALTT | |
| Human corona 229E pol 1ab (2854) | | LTGL---- | LPSSLKLVSTNLFEGDKFV | TFESA | AGT | |
| Murine hepatitis pol 1ab (3222) | | VS----- | NHALWLFSCYCRKLGTEVRS | DGTFEEM | ALTT | |
| Consensus (3277) | | VS | NHALWL | FKYCRKLGTVRS | VGTFEEMALTT | |
| Section 86 | | | | | | |
| | (3316) | 3316 | 3330 | 3340 | 3354 | |
| avian infectious bronchitis pol 1ab (2703) | | VIRGSEFV | ITREIG-DKDEA | LSAARLK | YEGTGSEQ | |
| bovine coronavirus pol 1ab (3168) | | MITKDSYCK | LKNSISDVAFNR | ISTNKYR | YSCKMDTA | |
| Human corona 229E pol 1ab (2889) | | VIDMRSYER | TANSTISPEKLS | AASNRYK | YSGHANEA | |
| Murine hepatitis pol 1ab (3255) | | M-TKESYCK | LKNSISDVAFNR | ISTNKYR | YSCKMDTA | |
| Consensus (3316) | | MITKDSYCK | LKNSISDV | KFNRYLSLYNKY | KYYS | |
| Section 87 | | | | | | |
| | (3355) | 3355 | 3360 | 3370 | 3380 | 3393 |
| avian infectious bronchitis pol 1ab (2741) | | DLOICRAW | YALDOYR | NSGVEIV | TPRYSIGV | RE |
| bovine coronavirus pol 1ab (3207) | | AAREACSO | LAKAMDTFTNNNGSDVL | QPTASVST | SEL | |
| Human corona 229E pol 1ab (2928) | | DTRCACYAY | LAKMLDFSRDHN | DTLT | TVSYG | STL |
| Murine hepatitis pol 1ab (3294) | | AAREACSO | LAKAMETENHNNNGNDVL | QPTASVTH | SET | |
| Consensus (3355) | | DYREACCA | QLAKAMDTFS | NNG | DILYTPPTAS | VGTSFL |
| Section 88 | | | | | | |
| | (3394) | 3394 | 3400 | 3410 | 3420 | 3432 |
| avian infectious bronchitis pol 1ab (2779) | | QSGFKALVS | SSA | TKELVSVS | RGNNNG | LWLGDTLY |
| bovine coronavirus pol 1ab (3246) | | QSGIV | MVNTSK | PTVS | TIGNMT | LNGLWLGDKV |
| Human corona 229E pol 1ab (2965) | | QAGLR | MAQPSGF | SKVVR | CLGNTV | ANGWLGIV |
| Murine hepatitis pol 1ab (3333) | | QSGIV | MVNTSK | PTVS | TIGNMT | LNGLWLGDKV |
| Consensus (3394) | | QSGIVKMV | SPSSKVEPCIVSVTYGNMT | LNGLWLGDKV | YC | |
| Section 89 | | | | | | |
| | (3433) | 3433 | 3440 | 3450 | 3460 | 3471 |
| avian infectious bronchitis pol 1ab (2818) | | PRHVLGKFSGDQWN | IVLN | ANNHEFEVTTQHG | --VT | LN |
| bovine coronavirus pol 1ab (3285) | | PRHVIC | SASDMTNP | PDYTNLLCRVTSSDFT | VLFDRLS | LT |
| Human corona 229E pol 1ab (3004) | | PRHVTASN | -TTSAIN | YDHEYSIMRLHNE | STISGTAF | GV |
| Murine hepatitis pol 1ab (3372) | | PRHVIC | SSADMTNP | PDYTNLLCRVTSSDFT | CVM | SGRMS |
| Consensus (3433) | | PRHVIC | SASDMT | PDY | NLLCRVTSSDFT | VISGRLSLTV |
| Section 90 | | | | | | |
| | (3472) | 3472 | 3480 | 3490 | 3500 | 3510 |
| avian infectious bronchitis pol 1ab (2855) | | VSRRRLK | AVLILQTA | VAANAEL | KKYKE | IKANCCDSPTIAC |
| bovine coronavirus pol 1ab (3324) | | MSYQMOG | CMLVLT | VTLQNSR | TPKYT | EGVVKPGETFTVLA |
| Human corona 229E pol 1ab (3042) | | VGATMH | GVTKIKVS | QTMH | TRHS | RTLKSL |
| Murine hepatitis pol 1ab (3411) | | MSYQMOG | CMLVLT | VTLQNPNT | FKYS | FSGVVKPGETFTVLA |
| Consensus (3472) | | MSYQMOG | CMLVLT | VTLQNA | TPKYSE | FGVVKPGETFTILA |

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FIGURE 4A (contd.)

| Section 91 | | | | |
|--|--------|---|------|-----------|
| | (3511) | 3511 | 3520 | 3530 3549 |
| avian infectious bronchitis pol 1ab (2894) | | A G T V V G L Y P T M R S N G T T R A S F L A F A C S V F N I E K G | | |
| bovine coronavirus pol 1ab (3363) | | A N G K P Q G A F H V T M R S S Y I I K G S F L C C S C G S V G Y V L M G D | | |
| Human corona 229E pol 1ab (3081) | | C D C A Q C V F G M M E T N W T I R G S I N L A K P Y N I K N G | | |
| Murine hepatitis pol 1ab (3450) | | A N R P Q G A F H T L S S H I K G C F L C S C S V V V L T G D | | |
| Consensus (3511) | | AYNGKPQGAFHVTMRSSWTIKGSFLCGACGSVGYVL GG | | |
| Section 92 | | | | |
| | (3550) | 3550 | 3560 | 3570 3588 |
| avian infectious bronchitis pol 1ab (2933) | | V N F F M H H L L P N A L H T G T D L M E E F C G Y V E E V A Q R V | | |
| bovine coronavirus pol 1ab (3402) | | C K E V M H O L E T S T G C H T G T D F N D F L G P Y K A Q V V Q L P | | |
| Human corona 229E pol 1ab (3120) | | E E V I N K O I L G S G S H V O S S F D V M I G F E Q P N L V E | | |
| Murine hepatitis pol 1ab (3489) | | S R E V I I O L F S T G C H T G T D F S C N E Y C P Y R A Q V V Q L P | | |
| Consensus (3550) | | VKFEVYMHQLELSTGCHTGTDF GDFYGPYKDAQVVQLP | | |
| Section 93 | | | | |
| | (3589) | 3589 | 3600 | 3610 3627 |
| avian infectious bronchitis pol 1ab (2972) | | P P D N I V T N M T V W L E A L I S V K E S S F S L P K W L E S T T V S V | | |
| bovine coronavirus pol 1ab (3441) | | V Q D Y I Q S V N F A R L E A A I L N N - - - - - C N W F V Q S D K C S V | | |
| Human corona 229E pol 1ab (3159) | | S A N Q M L T V V V A R L A A I L N G - - - - - C T W W L K G E K L F V | | |
| Murine hepatitis pol 1ab (3528) | | V Q D Y T O T V V V A W L A I L F N R - - - - - C N W F V Q S D S C S L | | |
| Consensus (3589) | | VQDYIQT VNVVAVLYAAILN C N W F L Q S D K C S V | | |
| Section 94 | | | | |
| | (3628) | 3628 | 3640 | 3650 3666 |
| avian infectious bronchitis pol 1ab (3011) | | D D Y M K T I G D I T P F F S T S T A T K S A I P S T D V C K L L R T I | | |
| bovine coronavirus pol 1ab (3474) | | E D F I V W A L S N G F S Q V K S D L V I D A L A S M T G S I E T L A A T | | |
| Human corona 229E pol 1ab (3192) | | E H Y L E N Q A N S T A M N G E D A F S I L A A K L T C V E R L L H A I | | |
| Murine hepatitis pol 1ab (3561) | | E E F N V W M T C G S S I K A D L V L D A L A S M T G T V E Q V I A A I | | |
| Consensus (3628) | | EDFNVWALSNGFSAIKADLVIDALAAMTGVSVEKLLAAI | | |
| Section 95 | | | | |
| | (3667) | 3667 | 3680 | 3690 3705 |
| avian infectious bronchitis pol 1ab (3050) | | M V K N S Q W G C D P D E Q Y N F E D E L T P E S V E N I G C V R Q C - | | |
| bovine coronavirus pol 1ab (3513) | | K R L K N G F Q R O T M S C S F E D E L T P S D V Y O L L A C I K C C K | | |
| Human corona 229E pol 1ab (3231) | | Q V L N N G E G G K Q I L G Y S S L N O F S I N E V V R M F G V N L Q S - | | |
| Murine hepatitis pol 1ab (3600) | | K R L H S G F Q K Q I L S C V L E D L T P S D V Y O L A G V K L Q S K | | |
| Consensus (3667) | | KVLNSGFQ GKQILGSCSLEDELTPSDVYQQLAGVKLQSK | | |
| Section 96 | | | | |
| | (3706) | 3706 | 3720 | 3730 3744 |
| avian infectious bronchitis pol 1ab (3088) | | - S F V R K A T S - W F W S R C V L A C T L F V L C A I V L F T A V P L K F Y | | |
| bovine coronavirus pol 1ab (3552) | | R T R L V K G I V C W I M A S T F L E S C I I T A F V K W T M F M Y V T T N M | | |
| Human corona 229E pol 1ab (3269) | | - G K T T S M F K S I S L F A G F F V M F W A E L F V Y T T T I W V N P G F L | | |
| Murine hepatitis pol 1ab (3639) | | R T R V I K G T C C W I L A S T F L F C S I I S A E V K W T M F M Y V T T H M | | |
| Consensus (3706) | | RTRVIKGT CWILASTFLFCFIISLFVKWTMFM YVTTFM | | |

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FIGURE 4A (contd.)

| Section 97 | | | | | | |
|--|--------|----------|--------------|-----------|------------|--------------------|
| | (3745) | 3745 | 3750 | 3760 | 3770 | 3783 |
| avian infectious bronchitis pol 1ab (3125) | | VYAAVIL | EMAVLE | ISFTV | VMAYMDT | ETLEPTTITVITIG |
| bovine coronavirus pol 1ab (3591) | | LSITTF | CAICV | ISLAMLIV | IKHLYLT | MYILEVLF |
| Human corona 229E pol 1ab (3307) | | TPFMILL | VALLSL | CLTFVVR | IKVLF | LQVFLI |
| Murine hepatitis pol 1ab (3678) | | EGVTICAL | CGFVST | AMLLIK | IKHLYLT | MYIMEVL |
| Consensus (3745) | | L | ITICLL | CLVSEF | AMLLV | KHKHLYLT |
| Section 98 | | | | | | |
| | (3784) | 3784 | 3790 | 3800 | 3810 | 3822 |
| avian infectious bronchitis pol 1ab (3164) | | VCAEMPF | FIYNTLIS | QVVIFLS | QWYDPVV | EDTMV |
| bovine coronavirus pol 1ab (3630) | | NYLVVYK | QTFRGYV | YAWLES | YYVPS | VEYTYT |
| Human corona 229E pol 1ab (3346) | | NCAWDYH | VTKVLA | EKF | DYNVSV | MMQDIO |
| Murine hepatitis pol 1ab (3717) | | NYLVVYK | QSF | RGLAYAW | ESHFVPA | VDYTYM |
| Consensus (3784) | | NYLVVYK | QTFRLI | AYAWLS | VSVPAVD | TYTDEVIY |
| Section 99 | | | | | | |
| | (3823) | 3823 | 3830 | 3840 | 3850 | 3861 |
| avian infectious bronchitis pol 1ab (3203) | | EVLYTA | FKCVQGCY | MNSFN | TSLMLYQ | FVKLG |
| bovine coronavirus pol 1ab (3669) | | ELGMVF | VTLRSINHD | ----- | LFSPIM | FVGRVIS |
| Human corona 229E pol 1ab (3385) | | ALLHTW | RFAKER | ----- | CTHWCTY | LFSLI |
| Murine hepatitis pol 1ab (3756) | | LVAMVF | VTLRSINHD | ----- | VFSIMF | LVGRIVS |
| Consensus (3823) | | LVL | MVFVTLRSINHD | ----- | LFSEI | LVGRIVS |
| Section 100 | | | | | | |
| | (3862) | 3862 | 3870 | 3880 | 3890 | 3900 |
| avian infectious bronchitis pol 1ab (3242) | | NTLTAY | TEGNWEL | FFELVHTTV | LANVSSNSLI | GLFVFKC |
| bovine coronavirus pol 1ab (3699) | | SLWYMG | SNLEEE | ILLMIAS | LF | GTYTWT |
| Human corona 229E pol 1ab (3409) | | AVLYTA | LYSYDYV | SLVMLL | CAISNEWY | TGATIFRICRF |
| Murine hepatitis pol 1ab (3786) | | SMWYF | GANLEEE | VLLFTT | SLFGTYTWT | TMLSDATAK |
| Consensus (3862) | | SLWY | GSNLEEE | VLLLLMSL | FGTYTWT | TILSIA |
| Section 101 | | | | | | |
| | (3901) | 3901 | 3910 | 3920 | | 3939 |
| avian infectious bronchitis pol 1ab (3281) | | AKWMLY | YCNA | TYLNNYV | LMAMVNC | IGWLCTC |
| bovine coronavirus pol 1ab (3738) | | KWVAVN | VLYFTD | IPQIKV | LVLCYLF | IGNTIS |
| Human corona 229E pol 1ab (3448) | | GVAFLP | VEYVS | YFDG | VKTVIL | FYMLL |
| Murine hepatitis pol 1ab (3825) | | KWLA | VNVLYFTD | VPOIKV | LVLLSY | LCIGYVCC |
| Consensus (3901) | | KWLA | VNVLYFTY | IPQIKV | LVLL | YLCIGYVCCCYWGLLSW |
| Section 102 | | | | | | |
| | (3940) | 3940 | 3950 | 3960 | | 3978 |
| avian infectious bronchitis pol 1ab (3320) | | VMKVFG | LTGKYN | FKVSV | VDQYR | MCCLHKL |
| bovine coronavirus pol 1ab (3777) | | MNSL | FRMPL | CVNYK | ISVQEL | RYMNANGLRPPKNSFEAL |
| Human corona 229E pol 1ab (3487) | | LRRECK | CTLC | VYDFCV | PAEFK | YLVANGLNARNGPF |
| Murine hepatitis pol 1ab (3864) | | LSL | FRMPL | CVNYK | ISVQEL | RYMNANGLRPPKNSFEAL |
| Consensus (3940) | | INSI | FRMTL | GVYNFK | ISVQEL | RYMNANGLRPPKNSFEAL |

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FIGURE 4A (contd.)

| Section 103 | | | | | | |
|--|--------|----------------|--------------------|-------------------|------------|------|
| | (3979) | 3979 | 3990 | 4000 | 4017 | |
| avian infectious bronchitis pol 1ab (3359) | | STNIIIOGCTGG | DRVLPATVCAKLS | IVCTTVVLMOLLT | | |
| bovine coronavirus pol 1ab (3816) | | MLNFKLLGIGG | VPIIEVSQFOSKLT | EVKCANVILNCLQ | | |
| Human corona 229E pol 1ab (3526) | | FIISEKLMELGG | PRTIKVSTVQSKT | TJLFCNTNVVIMGILS | | |
| Murine hepatitis pol 1ab (3903) | | MLNFKLLGIGG | VPVIEVSQLOSR | TDVRIANVILNCLQ | | |
| Consensus (3979) | | MLNFKLLGIGG | VRVIEVSTVQSKLT | TDVKCTNVVLLNCLQ | | |
| Section 104 | | | | | | |
| | (4018) | 4018 | 4030 | 4040 | 4056 | |
| avian infectious bronchitis pol 1ab (3398) | | KLNVEANSLMHV | LVEITHAKLASD | IVGECMDNLLGMILL | | |
| bovine coronavirus pol 1ab (3855) | | HLHVASNSKLWQ | CSTLIELLATS | DLGVAFEKLAOLIT | | |
| Human corona 229E pol 1ab (3565) | | NMNIASSTLEWA | CVEMENKINLCD | PETAQELLIALIA | | |
| Murine hepatitis pol 1ab (3942) | | HLHVASNSKLWQ | CSTLIELLATS | DLGVAFDKLAOLIT | | |
| Consensus (4018) | | HLNVIASNSKLWQ | YCVTLHNKILATS | DLGVAFDKLLQLLI | | |
| Section 105 | | | | | | |
| | (4057) | 4057 | 4070 | 4080 | 4095 | |
| avian infectious bronchitis pol 1ab (3437) | | TLECIDSTTD | ----- | LSEYCDILKRSTVI | SVTOEERS | |
| bovine coronavirus pol 1ab (3894) | | VLFANPAAVDSKCL | TSIEEVCD | DYAKDNTVLCALQSEFV | | |
| Human corona 229E pol 1ab (3604) | | FFLSKHSDFG | ----- | LGDLVSYFENDSIL | CSVASSTFV | |
| Murine hepatitis pol 1ab (3981) | | VLFANPAAVDSKCL | ASIEEVSD | DYVRDNTVLCALQSEFV | | |
| Consensus (4057) | | VLFANPAAVDSKCL | SIEEVCD | DYLDKNTVLCALQSEFV | | |
| Section 106 | | | | | | |
| | (4096) | 4096 | 4110 | 4120 | 4134 | |
| avian infectious bronchitis pol 1ab (3470) | | HTPZYAEYHRA | KNLYEKVLVDSKNGGVTO | ELAAAYRKA | | |
| bovine coronavirus pol 1ab (3933) | | NMAHFVHETVA | KNLDEARSSGSAN | ---QQLKOLEKAC | | |
| Human corona 229E pol 1ab (3637) | | GMPLEVALTET | ROEYENAVANGSS | ---PDILKQDKFAM | | |
| Murine hepatitis pol 1ab (4020) | | NMAHFVEYEL | KNLDEAKASGSAN | ---QQQIKOLEKAC | | |
| Consensus (4096) | | NMPSPVEYELAK | KNYDEARASGSAN | QQQIKOLEKAC | | |
| Section 107 | | | | | | |
| | (4135) | 4135 | 4140 | 4150 | 4160 | 4173 |
| avian infectious bronchitis pol 1ab (3509) | | NIAKSVFEDDLA | OKLDS | ERMTTINFA | VTDRRA | |
| bovine coronavirus pol 1ab (3969) | | NIAKSAYEEDRA | ARLER | DLALTNEYELAR | INDKKS | |
| Human corona 229E pol 1ab (3672) | | EVATAEFDDESS | VOKINP | AEQAAAT | TEARAVNRKS | |
| Murine hepatitis pol 1ab (4056) | | NIAKSAYEEDRA | ARLERMADL | LTNMYELAR | INDKKS | |
| Consensus (4135) | | NIAKSAFDRDRA | VQKKLERMADL | ALTNMYKEAR | INDKKS | |
| Section 108 | | | | | | |
| | (4174) | 4174 | 4180 | 4190 | 4200 | 4212 |
| avian infectious bronchitis pol 1ab (3548) | | KLVSSLHALLES | SLKKTLSEKLN | VLFDDQSS | CVVELATM | |
| bovine coronavirus pol 1ab (4008) | | KVVSALQTMLES | SMVRKLDNOAL | NSILDNAV | KCVPLNAT | |
| Human corona 229E pol 1ab (3711) | | KVVSAMHSLLEG | MLRRIMSSVD | TILNMARN | CVPLSVET | |
| Murine hepatitis pol 1ab (4095) | | KVVSALQTMLES | SMVRKLDNOAL | NSILDNAV | KCVPLNAT | |
| Consensus (4174) | | KVVSALQTLLES | MLRKLDNOAL | NSILDNAV | KGVVPLNAT | |

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FIGURE 4A (contd.)

| Section 109 | | | | | |
|--|--------|-----------------|------------------|---------------------------|------------------|
| | (4213) | 4213 | 4220 | 4230 | 4240 4251 |
| avian infectious bronchitis pol 1ab (3587) | | IVCSNR | TLVLPDPETWVKC | VEGVH | TLSTVNNIDTV |
| bovine coronavirus pol 1ab (4047) | | SLAANTLTITIV | EDKSVYDQVVDNVY | TTAGNV | QIOTT |
| Human corona 229E pol 1ab (3750) | | PATSAARTVVVVI | DHDSFVKMMVDGFVH | AGV | NTLQEV |
| Murine hepatitis pol 1ab (4134) | | SLTSNTLTITIV | LKOVFDQVVDNVY | TTAGN | MHTOFT |
| Consensus (4213) | | PSLSANTLTITIV | PKDVFVQVVDNVY | VTFYAGVVWNI | QITI |
| Section 110 | | | | | |
| | (4252) | 4252 | 4260 | 4270 | 4280 4290 |
| avian infectious bronchitis pol 1ab (3626) | | ITAGTELHPTST | TGSGLT | TYCISGANIAWF | KVNLTRNGH |
| bovine coronavirus pol 1ab (4086) | | QDSST | TNKQLNEISD | ----- | DCNWPVTIANRHNE |
| Human corona 229E pol 1ab (3789) | | KINDEGKNVHL | KDVTK | ----- | ENQEI VWPFLITCE |
| Murine hepatitis pol 1ab (4173) | | QDADGAVKOLNE | EDV | ----- | NSTWREIVTAANRHNE |
| Consensus (4252) | | QDADGTNKQLNEIS | | | NNWPLVI LNRHNE |
| Section 111 | | | | | |
| | (4291) | 4291 | 4300 | 4310 | 4329 |
| avian infectious bronchitis pol 1ab (3665) | | NKVDVVLO | NNELM | HGVKTKACVAGVDQAHCS | SVESKCY |
| bovine coronavirus pol 1ab (4116) | | VSATVLO | NNELM | PAKLKTQVVNS | -GPDQTCNTPTQCY |
| Human corona 229E pol 1ab (3819) | | RVYKIQ | --NNELM | PGKMKVKATKG | -EGDGGITSEGNAL |
| Murine hepatitis pol 1ab (4203) | | VSTVVLO | NNELM | OKLRTPQVVNS | -GSDMNCNTPTQCY |
| Consensus (4291) | | VSV VLO | NNELMPAKLKTQVVNS | G DA | CNTPTQCY |
| Section 112 | | | | | |
| | (4330) | 4330 | 4340 | 4350 | 4368 |
| avian infectious bronchitis pol 1ab (3704) | | TNISGNSVVA | ITSSNP | NLVASFLEA | NOTYVDID |
| bovine coronavirus pol 1ab (4153) | | NNSNNGKIVY | ILSDVDGL | YTKILKDD | NFVVLBLEDP |
| Human corona 229E pol 1ab (3855) | | NNEGGRAFMY | YVTTKPGM | YVKWEHDS | -VVTVELEP |
| Murine hepatitis pol 1ab (4240) | | NTTGTGKIVY | ILSDCDGL | YTKIVKED | NCVVLELD |
| Consensus (4330) | | NNSGGGKIVYAILSD | PGLKYTKILKDDGN | VVLELDPP | |
| Section 113 | | | | | |
| | (4369) | 4369 | 4380 | 4390 | 4407 |
| avian infectious bronchitis pol 1ab (3743) | | CKFGMKVG | VKVEV | LLMFI | KNTRSIVAGMLL |
| bovine coronavirus pol 1ab (4192) | | CKFTVQDV | KGLKIKY | LVVIGGNTLARGW | VETISSTVR |
| Human corona 229E pol 1ab (3893) | | CRVIDTPT | GPQIKY | LEVNLNNLR | EGALCYIGATVR |
| Murine hepatitis pol 1ab (4279) | | CKISVQDV | KGLKIKY | YFVIGGNTLARGW | VVGLISSTVR |
| Consensus (4369) | | CKFSVQDV | KGLKIKYLYFVKN | CNTLARGWVLGTISSTVR | |
| Section 114 | | | | | |
| | (4408) | 4408 | 4420 | 4430 | 4446 |
| avian infectious bronchitis pol 1ab (3782) | | LOSKGHET | EEVDAVGT | SLCS | FAVLEADTYCKYVAAQ |
| bovine coronavirus pol 1ab (4231) | | LQAG | -TATEYASNS | SILSLCAFS | DPKKTYLDFIQGGT |
| Human corona 229E pol 1ab (3932) | | LQAG | -KQTEFVSNS | SHLLTHCSLA | FAAAVLEDAVKQCAK |
| Murine hepatitis pol 1ab (4318) | | LQAG | -TATEYASNS | SAILSLCAFS | VDPKKTYLDYIKQGG |
| Consensus (4408) | | LQAG | TATEYVSNS | SAILSLCAFAVDPKKTYLDYIKQGG | |

FIGURE 4A (contd.)

| Section 115 | | | | |
|--|----------------|-----------------|----------------------|-----------------|
| | (4447) 4447 | 4460 | 4470 | 4485 |
| avian infectious bronchitis pol 1ab (3821) | LGNCVKMLTVHNS | SEPAIT | SKPSPTTDCPS | CGASVCI |
| bovine coronavirus pol 1ab (4269) | PIANMKMLCDHAGT | EMALTVKPDATTN | LSYGGASVCI | |
| Human corona 229E pol 1ab (3970) | EVGHCKMLTNGS | SSQMTTCTIDSM | TTDTYGGASVCI | |
| Murine hepatitis pol 1ab (4356) | PVTNCEMLTCDHA | TNMLIKPEATTN | QDSYGGASVCI | |
| Consensus (4447) | PVGNCVKMLTDHAG | SGMAITIKPDATTN | QDSYGGASVCI | |
| Section 116 | | | | |
| | (4486) 4486 | 4500 | 4510 | 4524 |
| avian infectious bronchitis pol 1ab (3860) | YCAHIAHFG | GSVGNLGRQFK | SEIITTEKDIVGFC | |
| bovine coronavirus pol 1ab (4308) | YCRARVEHL | -----DVDGLCKLR | KEVQVVGIKLVSYV | |
| Human corona 229E pol 1ab (4009) | YCAHVAH | -----TMHDFCQYKE | KWVVFIGTNDPIREC | |
| Murine hepatitis pol 1ab (4395) | YCRSRVEHL | -----DVDGLCKLR | KEVVLGKLVSYV | |
| Consensus (4486) | YCRARVEHP | | DVDGLCQLKGK | FVQVPIGKDPVSFV |
| Section 117 | | | | |
| | (4525) 4525 | 4530 | 4540 | 4550 4563 |
| avian infectious bronchitis pol 1ab (3899) | LRNKSTWQC | WIGYGC | ODSLRQPKSSVQSVAGASDF | |
| bovine coronavirus pol 1ab (4343) | LTNDVCQVCGF | WRDGS | SSVSTD | -----TTVQSKD |
| Human corona 229E pol 1ab (4044) | LENTCKVCGC | WLNHGCT | ODRT | -----AIQSF |
| Murine hepatitis pol 1ab (4430) | LTNDVCQVCGF | WRDGS | SSVGTG | -----SQFQSKD |
| Consensus (4525) | LTNDVCQVCGF | WRDGS | SSCVST | SAIQSKD |
| Section 118 | | | | |
| | (4564) 4564 | 4570 | 4580 | 4590 4602 |
| avian infectious bronchitis pol 1ab (3938) | KNYLNRVPLCS | -EARLTP | PLASCDPQVVKEL | EDVCKNES |
| bovine coronavirus pol 1ab (4373) | TNFLNRAVPLCS | -ASTSVDARLVPCAS | GLSTQVLA | APDIAASV |
| Human corona 229E pol 1ab (4072) | NSYLNRVPLCS | ---SARLEPCN | ETDIDYCV | ATPVYKDA |
| Murine hepatitis pol 1ab (4460) | TNFLNRVPLCS | SVNARLVPCAS | GLDTHVQV | APDIAANR |
| Consensus (4564) | TNFLNRVRGSS | VSDARLVPCAS | GLDTHVQV | APDIAANR |
| Section 119 | | | | |
| | (4603) 4603 | 4610 | 4620 | 4630 4641 |
| avian infectious bronchitis pol 1ab (3976) | AGMFQNLRRMCA | TFQELRDTEDGN | LEYLSSYFV | QOTTP |
| bovine coronavirus pol 1ab (4412) | AGIGLHL | VNCKRFQVDE | NGD | ----KLQFFVNRTDI |
| Human corona 229E pol 1ab (4109) | SFIGKNLS | SVFKNVDKD | -----AFYI | ARCIC |
| Murine hepatitis pol 1ab (4499) | AGIGLYYV | CCRFQVDE | EDGN | ----KLQFFVNRTDI |
| Consensus (4603) | AGIGLNLKVNCC | RFQVDE | EDGD | KLDAFFVVKRT L |
| Section 120 | | | | |
| | (4642) 4642 | 4650 | 4660 | 4670 4680 |
| avian infectious bronchitis pol 1ab (4015) | SNYEHEKSC | LEDLS | -EVTADLDE | EVFNKN---IYNISR |
| bovine coronavirus pol 1ab (4447) | TIYNFMECY | ERVNDCKFVA | EHD | ETTDVEGSRVPHIV |
| Human corona 229E pol 1ab (4140) | SVMDH | QSMNLL | GCNAVAKHDE | ETWHEGRTIYGNVSI |
| Murine hepatitis pol 1ab (4534) | EVYNKEKEC | ELTECGVVA | EHEE | ETEDVEGSRVPHIV |
| Consensus (4642) | SVYNHEKSCYELL | KDC | VVAEHD | ETFDVEGSRVPHIV |

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FIGURE 4A (contd.)

| Section 121 | | | | |
|--|-------------|-----------|------------|----------------------|
| | (4681) 4681 | 4690 | 4700 | 4719 |
| avian infectious bronchitis pol 1ab (4050) | QRHTKYTNM | FCYALHHP | PKDCEVLKE | ILVTYGCIEDY |
| bovine coronavirus pol 1ab (4486) | KDLTYTTL | LQYTHF | RNEGMLLCD | LSIYAGCEQS |
| Human corona 229E pol 1ab (4179) | QDLTKYTNM | LCEALRN | EEKDGEVFE | ILVTGCCSTD |
| Murine hepatitis pol 1ab (4573) | KDLSCELD | LQYALH | HELRNTCST | KEELTYAECRES |
| Consensus (4681) | QDLTKYTMLD | LCYALRHFD | RNDCEVLKEI | LVTYACCEDS |
| Section 122 | | | | |
| | (4720) 4720 | 4730 | 4740 | 4758 |
| avian infectious bronchitis pol 1ab (4089) | HPKWFEEN | DLYDPIEN | SKYYVMLAKM | PIVRRALLNAI |
| bovine coronavirus pol 1ab (4525) | Y---- | FTKIDLY | DFVENEDT | INVKKLPINR |
| Human corona 229E pol 1ab (4218) | Y---- | FEMNFF | PTFEDIHR | VYAALKVVAN |
| Murine hepatitis pol 1ab (4612) | Y---- | EOKDLY | DFVENEDT | INVKKLPINR |
| Consensus (4720) | Y | FEKKDWYD | PIENPDIIN | VKKLGPIVNR |
| Section 123 | | | | |
| | (4759) 4759 | 4770 | 4780 | 4797 |
| avian infectious bronchitis pol 1ab (4128) | EEGNLMYK | YCVTHDND | DKGKFG | EDFQKTARCA |
| bovine coronavirus pol 1ab (4560) | EEADKL | LEVLLV | ILVDMQD | NEKWTEDDYVIA |
| Human corona 229E pol 1ab (4253) | AACDEM | ILKVSE | VLQDNDN | NEYFCDFVLC |
| Murine hepatitis pol 1ab (4647) | KFADAL | EASLVH | LTLDND | LYGOWYFDFVKT |
| Consensus (4759) | EEFAD | LVEKGLV | GVLTLDN | QDLNGKFYDFGDFVKTAPGC |
| Section 124 | | | | |
| | (4798) 4798 | 4810 | 4820 | 4836 |
| avian infectious bronchitis pol 1ab (4167) | GVPVFD | TYEYMPIT | ATDAAP | RYFEYD-VHKGYS |
| bovine coronavirus pol 1ab (4599) | GVATADS | YSYNEM | LTCHALDC | LYVN-----NAYRL |
| Human corona 229E pol 1ab (4292) | CTPYCT | SYSEHVM | GTNCHAS | ECFMKSDIFGODEFT |
| Murine hepatitis pol 1ab (4686) | GVAVADS | YSYNEM | LTCHALDS | ELFVN-----GTYRE |
| Consensus (4798) | GVPVADS | YSYNMPML | TMTHALD | SELFVN D NAYKS |
| Section 125 | | | | |
| | (4837) 4837 | 4850 | 4860 | 4875 |
| avian infectious bronchitis pol 1ab (4205) | YFALKY | PYTEER | QELLQNY | PNYDQE |
| bovine coronavirus pol 1ab (4633) | FELVQ | LEFDYLL | EPNTHH | SMPPTNTVDCQDDRC |
| Human corona 229E pol 1ab (4331) | FDLLK | LDTEHKE | VLEN | PNYQD |
| Murine hepatitis pol 1ab (4720) | FELVQ | LEFDYLL | EPNTHH | SMTPTNTCEGLDRC |
| Consensus (4837) | FDLLQYD | FTDHKLE | LFNKYFKHWS | QDYHPNTVDC DDRC |
| Section 126 | | | | |
| | (4876) 4876 | 4890 | 4900 | 4914 |
| avian infectious bronchitis pol 1ab (4244) | LIHCAN | FNILEST | VIPIQIS | TCNLC |
| bovine coronavirus pol 1ab (4672) | LIHCAN | ENTLSM | VLENTCE | PIVQIVDGE |
| Human corona 229E pol 1ab (4370) | LIHCAN | ENTLSM | VLENTCE | PIVQIVDGE |
| Murine hepatitis pol 1ab (4759) | LIHCAN | ENTLSM | VLENTCE | PIVQIVDGE |
| Consensus (4876) | LIHCAN | FNILEST | VIPIQIS | TCNLC |

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FIGURE 4A (contd.)

| Section 127 | | | | | | |
|--|--------|----------------|--------------------|------------|------------|------------|
| | (4915) | 4915 | 4920 | 4930 | 4940 4953 | |
| avian infectious bronchitis pol 1ab (4283) | | YHSKEIGVIMQ | QNTMSFSKMGLSQ | LMQFVGL | LAALVGT | |
| bovine coronavirus pol 1ab (4711) | | YHYKELGIVMM | MDVTHRYRLSLKD | ILLYAADI | ALHVAS | |
| Human corona 229E pol 1ab (4409) | | YHEKQGLVW | NKLVNTHSTRLL | TITELLOFV | TFTTITAS | |
| Murine hepatitis pol 1ab (4798) | | YHYELGVMM | MDVTHRYRLSLKD | ILLYAADI | ALHVAS | |
| Consensus (4915) | | YHYKELGVMMNMDV | DTHRYRLSLKD | LLQFVAD | PALHVAS | |
| Section 128 | | | | | | |
| | (4954) | 4954 | 4960 | 4970 | 4980 4992 | |
| avian infectious bronchitis pol 1ab (4322) | | SNNIVLPLSL | SCALTS | LITHG | PECHFNKD | YDLA |
| bovine coronavirus pol 1ab (4750) | | ASALYDLRTCCFS | VAAITSGVKE | QTVKPGNF | NQDFYDFI | |
| Human corona 229E pol 1ab (4448) | | SFAVLEK | LVGLVAALST | LLTSQIVK | PECHFNKD | YDLA |
| Murine hepatitis pol 1ab (4837) | | ASALYDLRTCCFS | VAAITSGVKE | QTVKPGNF | NQDFYDFI | |
| Consensus (4954) | | ASALVDLRTCCFS | VAAITSGVTFQ | TVKPGNF | NQDFYDFI | |
| Section 129 | | | | | | |
| | (4993) | 4993 | 5000 | 5010 | 5020 5031 | |
| avian infectious bronchitis pol 1ab (4361) | | EKAEMFKG | CSIPNN | YPOTNAT | INDDY | YRIRPT |
| bovine coronavirus pol 1ab (4789) | | LSKGLLKEG | SSVDLKH | FFFTQD | GNAAITD | YNYYKYNRPT |
| Human corona 229E pol 1ab (4487) | | RSQFFDE | CELT | YITFTOKED | ELKEED | YRIRPT |
| Murine hepatitis pol 1ab (4876) | | LSKGLLKEG | SSVDLKH | FFFTQD | GNAAITD | YNYYKYNRPT |
| Consensus (4993) | | LSKGLLKEGSSVDL | KHFFFTQD | GNAAITD | YNYYKYNRPT | |
| Section 130 | | | | | | |
| | (5032) | 5032 | 5040 | 5050 | 5060 5070 | |
| avian infectious bronchitis pol 1ab (4400) | | MFDCLLFCLE | TSKPEC | EGGCPASQ | VVNNLDK | |
| bovine coronavirus pol 1ab (4828) | | MVDIKQLLFVLE | VVAKYFEI | YEGGCIPASQ | VIVNNYDKS | |
| Human corona 229E pol 1ab (4526) | | LLIGGARVAYQ | AARFDC | ELGLTSRE | VVTCLN | |
| Murine hepatitis pol 1ab (4915) | | MVDIKQLLFVLE | VVAKYFEI | YEGGCIPASQ | VIVNNYDKS | |
| Consensus (5032) | | MVDIKQLLFVLEV | VVAKYFEIYEGGCIPASQ | VIVNNYDKS | | |
| Section 131 | | | | | | |
| | (5071) | 5071 | 5080 | 5090 | 5109 | |
| avian infectious bronchitis pol 1ab (4439) | | AGYFFNFKG | KARLYYEALS | FEEQDEIF | AYTKRNVLP | TLT |
| bovine coronavirus pol 1ab (4867) | | AGYFFNFKG | KARLYYEALS | FEEQDEIF | AYTKRNVLP | TLT |
| Human corona 229E pol 1ab (4565) | | AGYFFNFKG | KARLYYEALS | FEEQDEIF | AYTKRNVLP | TLT |
| Murine hepatitis pol 1ab (4954) | | AGYFFNFKG | KARLYYEALS | FEEQDEIF | AYTKRNVLP | TLT |
| Consensus (5071) | | AGYFFNFKGKARLY | YEALSFEQDEIF | AYTKRNVLP | TLT | |
| Section 132 | | | | | | |
| | (5110) | 5110 | 5120 | 5130 | 5148 | |
| avian infectious bronchitis pol 1ab (4477) | | QMNLYAISA | KNRARTVAGV | SILSTMT | GRQFHQCK | LSI |
| bovine coronavirus pol 1ab (4906) | | QMNLYAISA | KNRARTVAGV | SILSTMT | GRQFHQCK | LSI |
| Human corona 229E pol 1ab (4604) | | QMNLYAISA | KNRARTVAGV | SILSTMT | GRQFHQCK | LSI |
| Murine hepatitis pol 1ab (4993) | | QMNLYAISA | KNRARTVAGV | SILSTMT | GRQFHQCK | LSI |
| Consensus (5110) | | QMNLYAISA | KNRARTVAGV | SILSTMT | GRQFHQCK | LSI |

FIGURE 4A (contd.)

| Section 133 | | | | |
|--|--------|------------------------------|---------------------|-------------------|
| | (5149) | 5149 | 5160 | 5170 5187 |
| avian infectious bronchitis pol 1ab (4516) | | VNTRNASVVLGTTTETGGGDNMLRNI | ICGV | EDPIHMGWD |
| bovine coronavirus pol 1ab (4945) | | AATGVPVATETTKFYGGWDMLRRLIKD | | DNEVVMGWD |
| Human corona 229E pol 1ab (4643) | | VATRNATVATETTKFYGGWDMLRRLIKD | | DSEVVMGWD |
| Murine hepatitis pol 1ab (5032) | | AATGVPVATETTKFYGGWDMLRRLIKD | | DSEVVMGWD |
| Consensus (5149) | | VATRNVPVVI | GTTKFYGGWDNMLRRLIKD | VDDPVLIMGWD |
| Section 134 | | | | |
| | (5188) | 5188 | 5200 | 5210 5226 |
| avian infectious bronchitis pol 1ab (4555) | | YPKCDRAMPNLLTAASLVFAR | ITNCG | SWSERIRIYN |
| bovine coronavirus pol 1ab (4984) | | YPKCDRAMPNILLIVSSSLVLR | HEA | TSQSDFRYLAN |
| Human corona 229E pol 1ab (4682) | | YPKCDRAMPNILLIVSSSLVLR | HEA | TSQSDFRYLAN |
| Murine hepatitis pol 1ab (5071) | | YPKCDRAMPNILLIVSSSLVLR | HEA | TSQSDFRYLAN |
| Consensus (5188) | | YPKCDRAMPNILLIVSSSLVLR | KHDS | CCS SDRFYRLAN |
| Section 135 | | | | |
| | (5227) | 5227 | 5240 | 5250 5265 |
| avian infectious bronchitis pol 1ab (4594) | | ECAGVLSITVLA | TGIVKPEETSSG | DATTAYANSVNI |
| bovine coronavirus pol 1ab (5023) | | ECAGVLSITVLA | TGIVKPEETSSG | DATTAYANSVNI |
| Human corona 229E pol 1ab (4721) | | ECAGVLSITVLA | TGIVKPEETSSG | DATTAYANSVNI |
| Murine hepatitis pol 1ab (5110) | | ECAGVLSITVLA | TGIVKPEETSSG | DATTAYANSVNI |
| Consensus (5227) | | ECAGVLSITVLA | TGIVKPEETSSG | DATTAYANSVNI |
| Section 136 | | | | |
| | (5266) | 5266 | 5280 | 5290 5304 |
| avian infectious bronchitis pol 1ab (4633) | | IQATSAIVARLLSVITRD | LVYDN | IKSLCYELQQVPRV |
| bovine coronavirus pol 1ab (5062) | | CQAVSANVCALMS | CNGNKIEDLSIRAL | KRLYSNVYRAD |
| Human corona 229E pol 1ab (4760) | | CQAVSANVCALMS | CNGNKIEDLSIRAL | KRLYSNVYRAD |
| Murine hepatitis pol 1ab (5149) | | CQAVSANVCALMS | CNGNKIEDLSIRAL | KRLYSNVYRAD |
| Consensus (5266) | | CQAVSANVCALMS | CNGNKIEDLSIRAL | KRLYSNVYRAD |
| Section 137 | | | | |
| | (5305) | 5305 | 5310 | 5320 5330 5343 |
| avian infectious bronchitis pol 1ab (4672) | | NVDPAFVSEFYEFLNKHFS | MMLISDDG | VVCYNSTYASKG |
| bovine coronavirus pol 1ab (5101) | | NVDPAFVSEFYEFLNKHFS | MMLISDDG | VVCYNSTYASKG |
| Human corona 229E pol 1ab (4799) | | NVDPAFVSEFYEFLNKHFS | MMLISDDG | VVCYNSTYASKG |
| Murine hepatitis pol 1ab (5188) | | NVDPAFVSEFYEFLNKHFS | MMLISDDG | VVCYNSTYASKG |
| Consensus (5305) | | NVDPAFVSEFYEFLNKHFS | MMLISDDG | VVCYNSTYASKG |
| Section 138 | | | | |
| | (5344) | 5344 | 5350 | 5360 5370 5382 |
| avian infectious bronchitis pol 1ab (4711) | | LVADTSGIREVLLYQNNVF | MA | DSTCNVPLIEKGPHEFC |
| bovine coronavirus pol 1ab (5140) | | YIANISAFQQVLYYQNNV | FMS | EAACWVEDINNGPHEFC |
| Human corona 229E pol 1ab (4838) | | YIANISAFQQVLYYQNNV | FMS | EAACWVEDINNGPHEFC |
| Murine hepatitis pol 1ab (5227) | | YIANISAFQQVLYYQNNV | FMS | EAACWVEDINNGPHEFC |
| Consensus (5344) | | YIANISAFQQVLYYQNNV | FMS | EAACWVEDINNGPHEFC |

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FIGURE 4A (contd.)

| Section 139 | | | | | |
|--|--------|---------|----------|------------|--------------------------|
| | (5383) | 5383 | 5390 | 5400 | 5410 5421 |
| avian infectious bronchitis pol 1ab (4750) | | SQHTMLV | EVVDGEPK | TEEFED | SRITIG CVPVVDVDLEEP |
| bovine coronavirus pol 1ab (5179) | | SQHTMLV | KMDGDDV | YLPYDP | SRILG GCFVDDLLKTD |
| Human corona 229E pol 1ab (4877) | | SQHTMQI | VDENGKY | LPYDP | SRISAGVVDLITLDA |
| Murine hepatitis pol 1ab (5266) | | SQHTMLV | KMDGDEV | YLPYDP | SRILG GCFVDDLLKTD |
| Consensus (5383) | | SQHTMLV | KMDGDDV | YLPYDP | SRILGAGVFVDDLLKTD |
| Section 140 | | | | | |
| | (5422) | 5422 | 5430 | 5440 | 5450 5460 |
| avian infectious bronchitis pol 1ab (4789) | | VAMM | YIATATE | NPVHLENEE | NKKVTFVLIAYIRK |
| bovine coronavirus pol 1ab (5218) | | VLLIERF | VSLAIDAY | PLVYHEN | PEYQKVERVYLEYIKK |
| Human corona 229E pol 1ab (4916) | | VLLIERY | VSLAIDAY | PLVYHEN | PEYQKVERVYLEYIKK |
| Murine hepatitis pol 1ab (5305) | | VLLIERF | VSLAIDAY | PLVYHEN | PEYQKVERVYLEYIKK |
| Consensus (5422) | | VLLIERF | VSLAIDAY | PLVYHEN | PEYQKVERVYLEYIKK |
| Section 141 | | | | | |
| | (5461) | 5461 | 5470 | 5480 | 5499 |
| avian infectious bronchitis pol 1ab (4828) | | YQELSON | MIMDY | EFVMDIDKGS | FWEQEYENMIRAPTT |
| bovine coronavirus pol 1ab (5257) | | YNDLGNQ | IILDSY | VILSTCDG | QKTDDETAKNMYLRSAV |
| Human corona 229E pol 1ab (4955) | | NKTINEG | VESFVTL | LDEHESK | FWDESTASLEKSTV |
| Murine hepatitis pol 1ab (5344) | | YNDLGNQ | IILDSY | VILSTCDG | QKTDDETAKNMYLRSAV |
| Consensus (5461) | | YNDLGNQ | IILDSY | VILSTCDG | SKFWDESTFYKNMYLRSTV |
| Section 142 | | | | | |
| | (5500) | 5500 | 5510 | 5520 | 5538 |
| avian infectious bronchitis pol 1ab (4867) | | LQSCVE | SHONSS | IRRCANOT | KEFLCCCOYTHVMH |
| bovine coronavirus pol 1ab (5296) | | MDSV | ACVFS | SCGSE | RGGSLIKKLLCCCOYTHVMH |
| Human corona 229E pol 1ab (4994) | | LQAAGL | AMG | SCVLR | GGDCLRMATLCAIDHAFGT |
| Murine hepatitis pol 1ab (5383) | | LQSVG | ACVFS | SCGSE | RGGSLIKKLLCCCOYTHVMH |
| Consensus (5500) | | LQSVG | ACVVCSS | QTSLR | CGSCIRKPLLCKCCYDHVMAT |
| Section 143 | | | | | |
| | (5539) | 5539 | 5550 | 5560 | 5577 |
| avian infectious bronchitis pol 1ab (4906) | | PHKNV | SINFL | ICSQLOG | GEAMVITATCGMSYFCGNIE |
| bovine coronavirus pol 1ab (5335) | | PHKYV | LSVSP | YVGNARG | LDVNDITATCGMSYFCEDHK |
| Human corona 229E pol 1ab (5033) | | PHKFL | IAITP | VCNTS | UNVNDITATCGMSYFCEDHK |
| Murine hepatitis pol 1ab (5422) | | PHKYV | LSVSP | YVGNARG | LDVNDITATCGMSYFCEDHK |
| Consensus (5539) | | PHKYV | LSIS | SPYVCNS | PGCDVNDVTKLYLGMSYFCEDHK |
| Section 144 | | | | | |
| | (5578) | 5578 | 5590 | 5600 | 5616 |
| avian infectious bronchitis pol 1ab (4945) | | PKLGIP | EVSNCT | ITCTYRANCA | SENVDDFNOLATTNWS |
| bovine coronavirus pol 1ab (5374) | | PQYSF | PKLVNMN | MYFGLY | KQSCTGSPYIDDFNKIASCKWT |
| Human corona 229E pol 1ab (5072) | | PHLSE | FPICSA | GNV | RGLYKSSALGMDIDVFKISTSDWS |
| Murine hepatitis pol 1ab (5461) | | PQYAF | PKLVNMN | MYFGLY | KQSCTGSPYIDDFNKIASCKWT |
| Consensus (5578) | | PQYSF | PPLVSN | GMVFG | LYKQSCTGSPYIDDFNKIASCKWS |

FIGURE 4A (contd.)

| Section 145 | | | | | |
|--|--|--------------------------|--------------|--------------|----------|
| (5617) | 5617 | 5630 | 5640 | 5655 | |
| avian infectious bronchitis pol 1ab (4984) | IVEP | IIANRCSDS | RRRLAEIVKLT | DELHQQFASAEV | |
| bovine coronavirus pol 1ab (5413) | DVDD | IIANECTERTKLE | ATTQATY | ATFOSYASATI | |
| Human corona 229E pol 1ab (5111) | DIRD | KLENDAKESTRLE | AAITVKE | SVISSYAYITL | |
| Murine hepatitis pol 1ab (5500) | EVDD | VLANECTERTKLE | ATTQATE | AEKQCYASATI | |
| Consensus (5617) | DVDDYILANECTESLKLFAAETVKATEEAFKQSYASATI | | | | |
| Section 146 | | | | | |
| (5656) | 5656 | 5670 | 5680 | 5694 | |
| avian infectious bronchitis pol 1ab (5023) | REIVFSDRRLILS | ULPGTREFI | NRHY | FNGYHEARTSKV | |
| bovine coronavirus pol 1ab (5452) | QELVSRRLILS | WEIGVKLLNKNYV | FNGYHFTKNGKT | | |
| Human corona 229E pol 1ab (5150) | KEIVGPKLLDL | LSQAKL | LNRRNS | CEQIKDSNF | |
| Murine hepatitis pol 1ab (5539) | REIVSDRELILS | WEIGVKLLNKNYV | FNGYHFTKNGKT | | |
| Consensus (5656) | REIVSDRELILSWEIGVKVPPPLNKNYVFTGYHFTKNSKT | | | | |
| Section 147 | | | | | |
| (5695) | 5695 | 5700 | 5710 | 5720 | 5733 |
| avian infectious bronchitis pol 1ab (5062) | QLGDFTEEGEGKDV | -VYKATSTAL | SVCDIFVL | SHN | |
| bovine coronavirus pol 1ab (5491) | VLGEYVVDSELNG | -VYRATTYKLSV | DVEVLTSHS | | |
| Human corona 229E pol 1ab (5189) | QVGEFVENVVDYGS | DTTKSTATT | LVPFML | ILSHN | |
| Murine hepatitis pol 1ab (5578) | VLGEYVVDSELNG | -VYRATTYKLSV | CDVFLDHA | | |
| Consensus (5695) | VLGEFVFDKSELNG | VYKATTTYKLSVGDVFILTSHN | | | |
| Section 148 | | | | | |
| (5734) | 5734 | 5740 | 5750 | 5760 | 5772 |
| avian infectious bronchitis pol 1ab (5100) | VVSLVAPTLCPQ | OTFSRFVNL | RPNVM | PECFVN | NIELH |
| bovine coronavirus pol 1ab (5529) | VANLSAPTLVPE | -NYSSIRFASVYS | LETFO | NVNV | Q |
| Human corona 229E pol 1ab (5228) | VAPLR | MANEKYSTIYK | HPSEN | VSDAYAN | LVFYQ |
| Murine hepatitis pol 1ab (5616) | VSSLSAPTLVPE | -NYTSIRFASVYS | PLETFO | NVNV | Q |
| Consensus (5734) | VASLSAPTLVPE | NYTSIRLASVYSVPETFO | NNVNPYQ | | |
| Section 149 | | | | | |
| (5773) | 5773 | 5780 | 5790 | 5800 | 5811 |
| avian infectious bronchitis pol 1ab (5139) | LVCKOKRTLVG | PPSTSHNFA | GLAVYESS | AVVFTAC | |
| bovine coronavirus pol 1ab (5567) | HIGMKRYCLV | GGPSTSHLA | GLAVCYCTA | VYTTAA | |
| Human corona 229E pol 1ab (5267) | LIGKQRITIT | LLGGSGHCS | IGVY | YPGAP | RTIC |
| Murine hepatitis pol 1ab (5654) | HIGMKRYCLV | GGPSTSHLA | GLAVYCTA | RVVYTTAA | |
| Consensus (5773) | LIGMQRYTTVQGGP | SGKSHLAIGLAVYYCTARVVFTAC | | | |
| Section 150 | | | | | |
| (5812) | 5812 | 5820 | 5830 | 5840 | 5850 |
| avian infectious bronchitis pol 1ab (5178) | SHAAVDALCEKA | HKFLKVD | CTRIV | QORTT | DCFSKFKA |
| bovine coronavirus pol 1ab (5606) | SHAAVDALCEKA | YKELNIND | CTRIVLAKVR | DCYDKFKI | |
| Human corona 229E pol 1ab (5306) | SHAAVDSLCAT | VTAYS | VOKGTS | ITARAR | EYSGLP |
| Murine hepatitis pol 1ab (5693) | SHAAVDALCEKA | HKFLNIND | CTRIVLAKVR | DCYDKFKI | |
| Consensus (5812) | SHAAVDALCEKAHKFLNINDCTRIVPAKVRVDCYSKFKI | | | | |

| | (5851) | 5851 | 5860 | 5870 | 5889 |
|--|--------|--------|--------|--------|--------|
| avian infectious bronchitis pol 1ab (5217) | NDTGKK | NDTGKK | NDTGKK | NDTGKK | NDTGKK |
| bovine coronavirus pol 1ab (5645) | NDTTRK | NDTTRK | NDTTRK | NDTTRK | NDTTRK |
| Human corona 229E pol 1ab (5345) | NNNSAQ | NNNSAQ | NNNSAQ | NNNSAQ | NNNSAQ |
| Murine hepatitis pol 1ab (5732) | NDTTRK | NDTTRK | NDTTRK | NDTTRK | NDTTRK |
| Consensus (5851) | NDTTRK | NDTTRK | NDTTRK | NDTTRK | NDTTRK |

| | (5890) | 5890 | 5900 | 5910 | 5928 |
|--|--------|--------|--------|--------|--------|
| avian infectious bronchitis pol 1ab (5256) | NGKINY | NGKINY | NGKINY | NGKINY | NGKINY |
| bovine coronavirus pol 1ab (5684) | NARTRA | NARTRA | NARTRA | NARTRA | NARTRA |
| Human corona 229E pol 1ab (5384) | NORISY | NORISY | NORISY | NORISY | NORISY |
| Murine hepatitis pol 1ab (5771) | NSRVSA | NSRVSA | NSRVSA | NSRVSA | NSRVSA |
| Consensus (5890) | NARISY | NARISY | NARISY | NARISY | NARISY |

| | (5929) | 5929 | 5940 | 5950 | 5967 |
|--|--------|--------|--------|--------|--------|
| avian infectious bronchitis pol 1ab (5294) | NDHVCV | NDHVCV | NDHVCV | NDHVCV | NDHVCV |
| bovine coronavirus pol 1ab (5723) | KLGLG | KLGLG | KLGLG | KLGLG | KLGLG |
| Human corona 229E pol 1ab (5423) | QRCAIG | QRCAIG | QRCAIG | QRCAIG | QRCAIG |
| Murine hepatitis pol 1ab (5810) | KLMCC | KLMCC | KLMCC | KLMCC | KLMCC |
| Consensus (5929) | KLMCC | KLMCC | KLMCC | KLMCC | KLMCC |

| | (5968) | 5968 | 5980 | 5990 | 6006 |
|--|--------|--------|--------|--------|--------|
| avian infectious bronchitis pol 1ab (5333) | PEERET | PEERET | PEERET | PEERET | PEERET |
| bovine coronavirus pol 1ab (5762) | ESSLC | ESSLC | ESSLC | ESSLC | ESSLC |
| Human corona 229E pol 1ab (5462) | EAKQ | EAKQ | EAKQ | EAKQ | EAKQ |
| Murine hepatitis pol 1ab (5849) | DNDSM | DNDSM | DNDSM | DNDSM | DNDSM |
| Consensus (5968) | EASSLC | EASSLC | EASSLC | EASSLC | EASSLC |

| | (6007) | 6007 | 6020 | 6030 | 6045 |
|--|--------|-------|-------|-------|-------|
| avian infectious bronchitis pol 1ab (5372) | RKKQ | RKKQ | RKKQ | RKKQ | RKKQ |
| bovine coronavirus pol 1ab (5798) | ANPLG | ANPLG | ANPLG | ANPLG | ANPLG |
| Human corona 229E pol 1ab (5498) | KNST | KNST | KNST | KNST | KNST |
| Murine hepatitis pol 1ab (5885) | ANPSW | ANPSW | ANPSW | ANPSW | ANPSW |
| Consensus (6007) | ANPSW | ANPSW | ANPSW | ANPSW | ANPSW |

| | (6046) | 6046 | 6060 | 6070 | 6084 |
|--|--------|------|------|------|------|
| avian infectious bronchitis pol 1ab (5411) | YDYV | YDYV | YDYV | YDYV | YDYV |
| bovine coronavirus pol 1ab (5837) | YDYV | YDYV | YDYV | YDYV | YDYV |
| Human corona 229E pol 1ab (5537) | YDYV | YDYV | YDYV | YDYV | YDYV |
| Murine hepatitis pol 1ab (5924) | YDYV | YDYV | YDYV | YDYV | YDYV |
| Consensus (6046) | YDYV | YDYV | YDYV | YDYV | YDYV |

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FIGURE 4A (contd.)

| Section 157 | | | | | |
|--|--------|---|-------|-------------------|-----------|
| | (6085) | 6085 | 6090 | 6100 | 6110 6123 |
| avian infectious bronchitis pol 1ab (5450) | | DELYSALKFTELDSETS | ----- | LOGTGEP | INKEFS |
| bovine coronavirus pol 1ab (5876) | | QLEFALQFTTLTLDKVPQAVETRVOCSTNLEKDCSKSYS | | | |
| Human corona 229E pol 1ab (5576) | | TLEDALKFFETITMDLQ | ----- | SESS-CGTFKDCARNPI | |
| Murine hepatitis pol 1ab (5963) | | QLFESLNFTTLTLDKIN | --- | NPRLOCTTN | LD SRSYV |
| Consensus (6085) | | QLFEALNFTTLTLDKIN | | RLQCSTNLEKDCSKSYS | |
| Section 158 | | | | | |
| | (6124) | 6124 | 6130 | 6140 | 6150 6162 |
| avian infectious bronchitis pol 1ab (5482) | | GVHFAAYVTTKALAATYVNDELAALVNVEAGSEITPKH | | | |
| bovine coronavirus pol 1ab (5915) | | GYHFAHAPSEFLAVDDKYKATGDI | | VCLGIGDS | AVTYSR |
| Human corona 229E pol 1ab (5609) | | DLPESHATTYDLSLDRFRTSGDI | | VOIGNNN | --VCLGEH |
| Murine hepatitis pol 1ab (5999) | | GYHFAHAPSEFLAVDDKYKVGDI | | VCLNVADS | AVTYSR |
| Consensus (6124) | | GYHFAHAPSEFLALDDKYKVSGLAVCLNVADS | | AVTYSR | |
| Section 159 | | | | | |
| | (6163) | 6163 | 6170 | 6180 | 6190 6201 |
| avian infectious bronchitis pol 1ab (5521) | | LISLLSKMSVNVEGCHNMFITRDEAIRN | | PGVGFIV | |
| bovine coronavirus pol 1ab (5953) | | LISLMGKLDVTLDTYCKLEIKKEE | | VKRPAVCEIAF | |
| Human corona 229E pol 1ab (5646) | | VITVMGTRFDVSMPSHSL | | CRDFAMRH | GLCMIV |
| Murine hepatitis pol 1ab (6037) | | LISLMGKLDLTLDTYCKLEITRDE | | IKRPAVCEIAF | |
| Consensus (6163) | | LISLMGFKLDVTLDTYCKLEITRDEAIKRVRAWVGFDVE | | | |
| Section 160 | | | | | |
| | (6202) | 6202 | 6210 | 6220 | 6230 6240 |
| avian infectious bronchitis pol 1ab (5560) | | GAHATRDSTGTFNELLQLEST | | LOEVEATLLEFADRDEY | |
| bovine coronavirus pol 1ab (5992) | | GAHATRDSTGTFNELLQLEST | | LOEVEATLLEFADRDEY | |
| Human corona 229E pol 1ab (5685) | | GAHVGGDNVGTNVELVGFENOVLE | | AOPEECVLINTGS | |
| Murine hepatitis pol 1ab (6076) | | GAHATRDSTGTFNELLQLEST | | LOEVEATLLEFADRDEY | |
| Consensus (6202) | | GAHATRDSTGTFNELLQLESTGIDFVVEPTGLVATRDGY | | | |
| Section 161 | | | | | |
| | (6241) | 6241 | 6250 | 6260 | 6279 |
| avian infectious bronchitis pol 1ab (5599) | | NFEFVNSKFAAGLQENLIRVFEKSAKPHHTIPPVQML | | | |
| bovine coronavirus pol 1ab (6031) | | SFKKAVAKAPPGQFKHLIPLMTRGOR | | DAVVPATVNTF | |
| Human corona 229E pol 1ab (5724) | | VVKFVRARAPPGQFQTHIVPLLRKGOP | | SILKKAVQMI | |
| Murine hepatitis pol 1ab (6115) | | VFKKAAARAPPGQFKHLIPLMTRGOR | | KWDVVRIPVQML | |
| Consensus (6241) | | VFKFV AKAPPGEQFKHLIPLMTRGORQPDVVRIPVQML | | | |
| Section 162 | | | | | |
| | (6280) | 6280 | 6290 | 6300 | 6318 |
| avian infectious bronchitis pol 1ab (5638) | | ADNLCMVSDCVVFTWCHGTELTTLRYFVKIGREV | | CCV | |
| bovine coronavirus pol 1ab (6070) | | ADNLCMVSDCVVFTWCHGTELTTLRYFVKIGREV | | CCV | |
| Human corona 229E pol 1ab (5763) | | ADFLAGSSVLFYLVAGGLELTTLRYFVKIGREV | | CCV | |
| Murine hepatitis pol 1ab (6154) | | SDHLADLANSVLTWAAASFELTCLRYFAVGREVVQSN | | | |
| Consensus (6280) | | ADHLADLSDCVVLTWAAAGLELTTLRYFVKIGREV | | CCV | |

| | (6319) | 6319 | 6330 | 6340 | 6357 | |
|--|--------|--|---------------------------------------|-------|----------------------------|--------|
| avian infectious bronchitis pol 1ab (5676) | | CGSRATTEFHHTQANA | TKKCLGF | FVY | LLVLISQWG | |
| bovine coronavirus pol 1ab (6109) | | CTKRATAYNERTGY | GQWRHSVTC | YL | ALLIVDTQWGC | |
| Human corona 229E pol 1ab (5801) | | CGTVATCYNEVSND | CCFKHALGCCYV | Y | YVIDLQWGC | |
| Murine hepatitis pol 1ab (6193) | | CTKRATCFNERTGY | GQWRHSYSCLYL | Y | ALLIVDTQWGC | |
| Consensus (6319) | | CTKRATCFNSRTGYYGCWKHSLGCDYLYNPLIVDIQQWG | | | | |
| Section 164 | | | | | | |
| | (6358) | 6358 | 6370 | 6380 | 6396 | |
| avian infectious bronchitis pol 1ab (5715) | | YSONIQF | DLHCH | IGHAN | YV | |
| bovine coronavirus pol 1ab (6148) | | IES | SS | DIYIS | LKGAHVASSDA | |
| Human corona 229E pol 1ab (5840) | | YV | SLST | HAITN | IRNE | |
| Murine hepatitis pol 1ab (6232) | | YTISITS | HDPTC | SL | LKGAHVASSDA | |
| Consensus (6358) | | YTGSLSSNHDLICSVHKGAAHVASSDAIMTRCLAVYDCFC | | | | |
| Section 165 | | | | | | |
| | (6397) | 6397 | 6410 | 6420 | 6435 | |
| avian infectious bronchitis pol 1ab (5754) | | QDVN | DLT | PHIAN | DEV | |
| bovine coronavirus pol 1ab (6187) | | NNIN | NVE | IT | S | |
| Human corona 229E pol 1ab (5879) | | KNVD | SIT | EMIA | ENAT | |
| Murine hepatitis pol 1ab (6271) | | KSVN | NLE | PLIS | Y | |
| Consensus (6397) | | KNVNWNLTYPPIANELSINTSCRLLQVRMLRAAMLCNRY | | | | |
| Section 166 | | | | | | |
| | (6436) | 6436 | 6450 | 6460 | 6474 | |
| avian infectious bronchitis pol 1ab (5793) | | NVVD | IGNCK | GI | KCVR | |
| bovine coronavirus pol 1ab (6226) | | TLCY | IGNEK | --- | AIAC | |
| Human corona 229E pol 1ab (5918) | | KAIH | IGNEK | --- | GIRCA | |
| Murine hepatitis pol 1ab (6310) | | DVCY | IGNCK | --- | GLAC | |
| Consensus (6436) | | VCYDIGNPK | | | AIACVKDFDEKFDKNPIVKS VKTLE | |
| Section 167 | | | | | | |
| | (6475) | 6475 | 6480 | 6490 | 6500 | 6513 |
| avian infectious bronchitis pol 1ab (5831) | | LDYNQ | HKDKF | ADLC | ME | EN |
| bovine coronavirus pol 1ab (6262) | | YSFEA | HKDSEK | ADLC | ME | EN |
| Human corona 229E pol 1ab (5955) | | LDYMT | AG | --- | QMB | GLCL |
| Murine hepatitis pol 1ab (6346) | | KRYEA | HKDQEL | ADLC | ME | EN |
| Consensus (6475) | | YDYEAHKD | FLDGLCMFWNCNVDPNAVVCREFDTRVL | | | |
| Section 168 | | | | | | |
| | (6514) | 6514 | 6520 | 6530 | 6540 | 6552 |
| avian infectious bronchitis pol 1ab (5870) | | SVF | PLPG | CNGG | SLYVN | KHAFHT |
| bovine coronavirus pol 1ab (6301) | | NNL | PLPG | CNGG | SLYVN | KHAFHT |
| Human corona 229E pol 1ab (5992) | | SIT | ME | ECV | IG | SYVN |
| Murine hepatitis pol 1ab (6385) | | NKL | PLPG | CNGG | SLYVN | KHAFHT |
| Consensus (6514) | | S | LNLPGCNGGSLYVNKHAFHTPPFDRAAFENLKPMPEF | | | |

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FIGURE 4A (contd.)

| Section 169 | | | | | |
|--|--------|---------|------------------|--------------|--------------------|
| | (6553) | 6553 | 6560 | 6570 | 6580 6591 |
| avian infectious bronchitis pol 1ab (5909) | | FIDSSP | ETIQVDGVAQ- | DLVSLATKD | DTTKCETLAVV |
| bovine coronavirus pol 1ab (6340) | | YLSDTF | VYMDGMDAKQVDY | YPTKSA | TCLELREKLEGAVC |
| Human corona 229E pol 1ab (6031) | | YEDDGS | EVVHDQVN---- | YPLRATN | CTUKITCCVVC |
| Murine hepatitis pol 1ab (6424) | | YLSDTF | VYMEGME | SKQVDY | YPLRSATCTIRNLGKALG |
| Consensus (6553) | | YYSDTF | PCVYMDGMDAKQVDY | VPLRSATC | ITKCNIGGAVC |
| Section 170 | | | | | |
| | (6592) | 6592 | 6600 | 6610 | 6620 6630 |
| avian infectious bronchitis pol 1ab (5947) | | KRIIAQM | YAEFVTSZAAVTS | CTTFV | TNKLNPAILTKS |
| bovine coronavirus pol 1ab (6379) | | LKHAEE | REYLESYNTATT | CTTFV | VYKTEDEFYNLNTL |
| Human corona 229E pol 1ab (6066) | | SKIAANL | RAYVECTIIFTQ | QENIW | PTTEDCMLTQIT |
| Murine hepatitis pol 1ab (6463) | | LKHAEE | REYLESYNTATT | CTTFV | VYKTEDEFYNLNTL |
| Consensus (6592) | | LKHAEE | YREYLESYNTATT | AGETFWV | YKTFDFYNLWNTF |
| Section 171 | | | | | |
| | (6631) | 6631 | 6640 | 6650 | 6669 |
| avian infectious bronchitis pol 1ab (5986) | | SAL-- | STDA | LAYMYKGGHYDA | IACEMTVITGD |
| bovine coronavirus pol 1ab (6418) | | TKL-- | SLEAVVY | LVKTEHYTGQAG | LMPCATINDVA |
| Human corona 229E pol 1ab (6105) | | TKL-- | GLEIAF | VVNKCEVGAD | ELPVATSGDVFV |
| Murine hepatitis pol 1ab (6502) | | TKL-- | SLEAVVY | LVNACHEDGR | ACELFCAVIGEKVIA |
| Consensus (6631) | | TKL | QSENI | VYNLVNAGHFDG | AGELPCAIIIGDKVFV |
| Section 172 | | | | | |
| | (6670) | 6670 | 6680 | 6690 | 6708 |
| avian infectious bronchitis pol 1ab (6023) | | IDQGV | EKAFFVQTLT | SVF | FYYAENIRTLNNRIL |
| bovine coronavirus pol 1ab (6455) | | KIDK | EDVVEFTIN | TYTNV | VLEFAEESIRHH |
| Human corona 229E pol 1ab (6144) | | RDGN | TDNLVVNK | SLEINLAF | EFAR |
| Murine hepatitis pol 1ab (6539) | | KIQNE | DVVVKN | TPFTNV | VLEFAEESIRPH |
| Consensus (6670) | | KIQNE | DVVVFVNNTTL | PTNVAVELE | FAKRSIRHPELKIL |
| Section 173 | | | | | |
| | (6709) | 6709 | 6720 | 6730 | 6747 |
| avian infectious bronchitis pol 1ab (6062) | | KG | GV | DTNGF | TMLANQTPLYRN |
| bovine coronavirus pol 1ab (6494) | | RNL | NIDVCWKH | IIND | ARESI |
| Human corona 229E pol 1ab (6183) | | KN | GV | VATYKFLMT | EAERELTSF |
| Murine hepatitis pol 1ab (6578) | | RNL | NIDVCW | SHVLE | AKDSVFCSS |
| Consensus (6709) | | KNLN | IDVTWKHVIWDY | AKESPLCS | NTYKVCA |
| Section 174 | | | | | |
| | (6748) | 6748 | 6760 | 6770 | 6786 |
| avian infectious bronchitis pol 1ab (6099) | | NGLV | VLYDDRY | DYOSTLAADNA | LVSTQCYN |
| bovine coronavirus pol 1ab (6533) | | KENV | LEDGRDNGALEA | KRSN | IGYISTTKV |
| Human corona 229E pol 1ab (6220) | | DVCT | CYDNSIOCSYER | ETLSTNA | VLESATAV |
| Murine hepatitis pol 1ab (6617) | | SLNV | LEDGRDNGALEA | KKCRNG | YINTTKT |
| Consensus (6748) | | LNV | LEDGRDNGAYEAFKKS | NAVYI | STTKVKSLSMIKG |

FIGURE 4A (contd.)

| Section 175 | | | | | | |
|--|--------|--|------|----------------|-----------|-----------------------|
| | (6787) | 6787 | 6800 | 6810 | 6825 | |
| avian infectious bronchitis pol 1ab (6138) | | PSNLLVQNGMPLKDCAN----- | | | LYVYKRVN- | |
| bovine coronavirus pol 1ab (6572) | | PPRAEINGVVVDKVGDTDCVFFYFAVRKEGQDVIFSOQDS | | | | |
| Human corona 229E pol 1ab (6257) | | LPAIKLNFQMINGNAIATVKSEDGNINWFEVYVRKDG | | | | |
| Murine hepatitis pol 1ab (6656) | | PQRADLNGVYVEKVGDSDFWFFAVRKDGDDVIFSRGDS | | | | |
| Consensus (6787) | | PPRADLNGVMVDKVGDSDFWFFAVRKDGNDVIFSR DS | | | | |
| Section 176 | | | | | | |
| | (6826) | 6826 | 6840 | 6850 | 6864 | |
| avian infectious bronchitis pol 1ab (6163) | | ----- | | GAFVTLPTNTN | IGSY | |
| bovine coronavirus pol 1ab (6611) | | LRVSSNQSPQGNLGSNEPGNVGNDALATSTIE | | | QSRVI | |
| Human corona 229E pol 1ab (6286) | | KPVDDHYDG----- | | | FYLGNTI | |
| Murine hepatitis pol 1ab (6695) | | LEPSHYRSPOGNPGGNRVGDI | | SGNEALARGTITFT | STLL | |
| Consensus (6826) | | L VSHY SPQGN G N G L GNDALA | | | TIFTQSRLL | |
| Section 177 | | | | | | |
| | (6865) | 6865 | 6870 | 6880 | 6890 | 6903 |
| avian infectious bronchitis pol 1ab (6180) | | ETTEPSTIRHILAMSEESTVERIG-KLGLQIIL | | | | E |
| bovine coronavirus pol 1ab (6650) | | SSFTCTDMEKDFLALDDDDFIQKYGLEDYAFEHIVYGN | | | | |
| Human corona 229E pol 1ab (6312) | | QDFLPSTMEELINMDIGVEIQKGLDFNEEFVVFED | | | | |
| Murine hepatitis pol 1ab (6734) | | SSFTPTSEMERKDFLMDIDDDVETAKSLQYAFELVVFES | | | | |
| Consensus (6865) | | SSFTPRSDMEKDFLALDDDDVFIQKYGLEDYAFEHIVYGD | | | | |
| Section 178 | | | | | | |
| | (6904) | 6904 | 6910 | 6920 | 6930 | 6942 |
| avian infectious bronchitis pol 1ab (6218) | | VDRPQDCEFTVIFGMYLLRANKENAKSVTNSDSVMQN | | | | |
| bovine coronavirus pol 1ab (6689) | | FNOKLIEFHLIGLYRQOTSNLVIOEFPVSYSSTHSY | | | | |
| Human corona 229E pol 1ab (6351) | | VSKTTLFHLISQVNLKMGILKAEEFVAASDITLKC | | | | |
| Murine hepatitis pol 1ab (6773) | | FNOKLIGGHLIGLALROOKSNLVIOEFPVYDSSTHSY | | | | |
| Consensus (6904) | | VNOKIIGGLHLLIGLYRRQQ | | | | SNLVIQEFVSYSSTHSY |
| Section 179 | | | | | | |
| | (6943) | 6943 | 6950 | 6960 | 6970 | 6981 |
| avian infectious bronchitis pol 1ab (6257) | | MFVLSDNQ-SYKQ | | | | FLVLLFHLHLLRNILKEYGTN |
| bovine coronavirus pol 1ab (6728) | | ELTDEKSG-GSKSVCTVIDLLHDFVALVRSLNLCVS- | | | | |
| Human corona 229E pol 1ab (6390) | | CTVTYLNDPSSSTVCTYMBLLHDFVSVLKEIDDTVVS- | | | | |
| Murine hepatitis pol 1ab (6812) | | ELTDENSG-SSKSVCTVIDLLHDFVDIVKSLNLCVS- | | | | |
| Consensus (6943) | | FIVDE SG SSKSVCTVIDLLLDFFVELLKSLLNLCVS | | | | |
| Section 180 | | | | | | |
| | (6982) | 6982 | 6990 | 7000 | 7010 | 7020 |
| avian infectious bronchitis pol 1ab (6295) | | KSKVVTMSIDYHSINFETWFEDGSIKTCTFQLOS--ANT | | | | |
| bovine coronavirus pol 1ab (6765) | | --KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLOAAADWK | | | | |
| Human corona 229E pol 1ab (6428) | | --KHEVILNKPWRWMLCKDNAVATFQFQLOS-AEHWK | | | | |
| Murine hepatitis pol 1ab (6849) | | --KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLOAAADWK | | | | |
| Consensus (6982) | | KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLOAAADWK | | | | |

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FIGURE 4A (contd.)

| Section 181 | | | | | | | |
|--|--------|-------------------------|-----------------|-----------|----------------|---------|---|
| | (7021) | 7021 | 7030 | 7040 | 7059 | | |
| avian infectious bronchitis pol 1ab (6332) | | CGNNLEEDY | VONCVM | PCNIPN | EVGITLPS | ILMVA | |
| bovine coronavirus pol 1ab (6802) | | PGSSLEVLK | YLNSEMERVSLW | LEKPVTLPT | GCMMN | VA | |
| Human corona 229E pol 1ab (6464) | | CGSSLEGI | KTORMCL | PCNLY | IGAGLKL | PSGIMFN | V |
| Murine hepatitis pol 1ab (6886) | | PGYVLEVL | YLESPLLRVNLW | NYCKPITI | PTGCMN | VA | |
| Consensus (7021) | | PGYSMPVLYKYQNSPLERVNLWN | YGKPITLPSGIMMNV | | | | |
| Section 182 | | | | | | | |
| | (7060) | 7060 | 7070 | 7080 | 7098 | | |
| avian infectious bronchitis pol 1ab (6371) | | KYTQELQYLSKPHIC | VPHNMRVHL | LGAGSDKG | VAPGSAV | | |
| bovine coronavirus pol 1ab (6841) | | KYQELQYLSKPHIC | VPHNMRVHL | LGAGSDKG | VAPGSAV | | |
| Human corona 229E pol 1ab (6503) | | KYTQELQYLSKPHIC | VPHNMRVHL | LGAGSDKG | VAPGSAV | | |
| Murine hepatitis pol 1ab (6925) | | KYTQELQYLSKPHIC | VPHNMRVHL | LGAGSDKG | VAPGSAV | | |
| Consensus (7060) | | KYTQELQYLS | TTTTLCVPHNMRVHL | LGAGSDKG | VAPGSAV | | |
| Section 183 | | | | | | | |
| | (7099) | 7099 | 7110 | 7120 | 7137 | | |
| avian infectious bronchitis pol 1ab (6410) | | LKQWL | PAGTILVDNDV | VPFVSD | AVASYFGDCITL | PFDCQ | |
| bovine coronavirus pol 1ab (6880) | | LKQWL | PAGTILVDNDV | VPFVSD | AVASYFGDCITL | PFDCQ | |
| Human corona 229E pol 1ab (6542) | | LKQWL | PAGTILVDNDV | VPFVSD | AVASYFGDCITL | PFDCQ | |
| Murine hepatitis pol 1ab (6964) | | LKQWL | PAGTILVDNDV | VPFVSD | AVASYFGDCITL | PFDCQ | |
| Consensus (7099) | | LKQWL | PAGTILVDNDV | VPFVSD | AVASYFGDCITL | PFDCQ | |
| Section 184 | | | | | | | |
| | (7138) | 7138 | 7150 | 7160 | 7176 | | |
| avian infectious bronchitis pol 1ab (6449) | | FDLIISDMYDP | ITKNIGEYNVSK | ---- | DGFFTYICH | FIR | |
| bovine coronavirus pol 1ab (6919) | | FDLIISDMYDP | ITKNIGEYNVSK | ---- | DGFFTYICH | FIR | |
| Human corona 229E pol 1ab (6581) | | FDLIISDMYDP | ITKNIGEYNVSK | ---- | DGFFTYICH | FIR | |
| Murine hepatitis pol 1ab (7003) | | FDLIISDMYDP | ITKNIGEYNVSK | ---- | DGFFTYICH | FIR | |
| Consensus (7138) | | FDLIISDMYDP | ITKNIGEYNVSK | ---- | DGFFTYICH | FIR | |
| Section 185 | | | | | | | |
| | (7177) | 7177 | 7190 | 7200 | 7215 | | |
| avian infectious bronchitis pol 1ab (6488) | | DKLALGGSVAIKITEFSWNAEL | YDL | MQKFAFWT | TMFCTNV | | |
| bovine coronavirus pol 1ab (6954) | | DKLALGGSVAIKITEFSWNAEL | YDL | MQKFAFWT | TMFCTNV | | |
| Human corona 229E pol 1ab (6616) | | DKLALGGSVAIKITEFSWNAEL | YDL | MQKFAFWT | TMFCTNV | | |
| Murine hepatitis pol 1ab (7038) | | DKLALGGSVAIKITEFSWNAEL | YDL | MQKFAFWT | TMFCTNV | | |
| Consensus (7177) | | DKLALGGSVAIKITEFSWNAEL | YDL | MQKFAFWT | TMFCTNV | | |
| Section 186 | | | | | | | |
| | (7216) | 7216 | 7230 | 7240 | 7254 | | |
| avian infectious bronchitis pol 1ab (6527) | | NASSSEAF | LIGINYL | G K | KVEIDGNTMHANYL | FWRNS | |
| bovine coronavirus pol 1ab (6993) | | NASSSEAF | LIGINYL | G K | KVEIDGNTMHANYL | FWRNS | |
| Human corona 229E pol 1ab (6655) | | NASSSEAF | LIGINYL | G K | KVEIDGNTMHANYL | FWRNS | |
| Murine hepatitis pol 1ab (7077) | | NASSSEAF | LIGINYL | G K | KVEIDGNTMHANYL | FWRNS | |
| Consensus (7216) | | NASSSEAF | LIGINYL | G K | KVEIDGNTMHANYL | FWRNS | |

FIGURE 4A (contd.)

| | | | | | | Section 187 |
|--|--------|-----------|----------------|------------|-----------------|-----------------|
| | (7255) | 7255 | 7260 | 7270 | 7280 | 7293 |
| avian infectious bronchitis pol 1ab (6565) | | NYLOTSAY | TFVAK | DERLKATP | VNEKTEOKTDL | FN |
| bovine coronavirus pol 1ab (7030) | | TVWNGGAYS | IFDMAK | PLKLAGIA | TINLRADOINDM | WYS |
| Human corona 229E pol 1ab (6694) | | TVMSLSYN | SVLLLS | NCKHKATV | VVO | KDS |
| Murine hepatitis pol 1ab (7114) | | TVWNGGAYS | IFDMAK | PLKAGTA | VVSHKPDQINDL | LS |
| Consensus (7255) | | TVWNGSAYS | LFDMAK | FPLKLKATAV | VNLK | DQINDLVLS |
| | | | | | | Section 188 |
| | (7294) | 7294 | 7300 | 7319 | | |
| avian infectious bronchitis pol 1ab (6604) | | LIEKGLI | VRDVGNTSETSDS | FNCTM | SEQ ID NO: 9905 | |
| bovine coronavirus pol 1ab (7069) | | LIEKGLI | VRDTNKEVEVGDSL | NVI | SEQ ID NO: 9886 | |
| Human corona 229E pol 1ab (6733) | | LIVRSGLI | VGNGKCLSF | SNHL | STK | SEQ ID NO: 9914 |
| Murine hepatitis pol 1ab (7153) | | LIEKGLI | VRDTRKEVEVGDSL | NVVK | SEQ ID NO: 9887 | |
| Consensus (7294) | | LIEKGLI | VRDTGKEVFVSDSL | NVVK | | |

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FIGURE 4B

| | | Section 1 | | | | |
|--------------------------------------|-------|---|-----|-----|-----|-----|
| | | (1) | 1 | 10 | 20 | 39 |
| human coronavirus OC43 NP | (1) | MSFTPGKQSSS-RASSGNRSGN-ILK---WADQSDQVRN | | | | |
| Bovine corona NP | (1) | MSFTPGKQSSS-RASFGNRSGN-ILK---WADQSDQSRN | | | | |
| avian infectious bronchitis virus NP | (1) | -----MASEKAAG--KSDSP--AP- | | | | |
| mouse hepatitis virus NP | (1) | MSEVPGQENAGGRSSSVNRAGN-ILKKTTFWADQTERGPN | | | | |
| Consensus | (1) | MSFTPGKQSSS RASSGNRSGNGILK WADQSDQARN | | | | |
| | | Section 2 | | | | |
| | | (40) | 40 | 50 | 60 | 78 |
| human coronavirus OC43 NP | (36) | VQTRGRRRAQ-LOTATSQQPSGGNVVPYY-HHSGITQFQK | | | | |
| Bovine corona NP | (36) | VQTRGRRRAQ-LOTATSQLPSSGGNVVPYY-HHSGITQFQK | | | | |
| avian infectious bronchitis virus NP | (16) | TIKLGPKP-IVGSSGN-----AL-QLAKAKKL | | | | |
| mouse hepatitis virus NP | (40) | NQNRGRNO-PKOTATTO-PNSGGSVVRHY-HHSGITQFQK | | | | |
| Consensus | (40) | VQTRGRRRAQPKQTATSQ PSGGNVVPYYSWFSGITQFQK | | | | |
| | | Section 3 | | | | |
| | | (79) | 79 | 90 | 100 | 117 |
| human coronavirus OC43 NP | (75) | GKEFEFV-COLPIAPGVPA-TEAK-LYYHNHRS-STAD | | | | |
| Bovine corona NP | (75) | GKEFEFV-COLPIAPGVPA-TEAK-LYYHNHRS-STAD | | | | |
| avian infectious bronchitis virus NP | (45) | NAPAPKE-LSSEVDNENLKN-SCQH-WRQAL---PGK | | | | |
| mouse hepatitis virus NP | (78) | GKEFEFV-COLPIANGIPASEQ-KLYYHNHRS-STAD | | | | |
| Consensus | (79) | GKEFEFAEGQGVPIAPGVPA-SEQKGYWYRHNHRSFKTAD | | | | |
| | | Section 4 | | | | |
| | | (118) | 118 | 130 | 140 | 156 |
| human coronavirus OC43 NP | (114) | GNORQLPR-FWYLLGTGPHAKDQY-GTDL-DVY-VASNQ | | | | |
| Bovine corona NP | (114) | GNORQLPR-FWYLLGTGPHAKDQY-TDID-VERV-VASNQ | | | | |
| avian infectious bronchitis virus NP | (82) | GGRAKVPDA-FLTETTCFANDLNW-DSQD-IV-VAAKQ | | | | |
| mouse hepatitis virus NP | (117) | GNORQLPR-FWYLLGTGPHAKDQY-GTDL-DVY-VASNQ | | | | |
| Consensus | (118) | GNQKQLLPRWYFYLLGTGPHAKDQY-GTSDGVFWVASNQ | | | | |
| | | Section 5 | | | | |
| | | (157) | 157 | 170 | 180 | 195 |
| human coronavirus OC43 NP | (153) | ADVNTPADIVDRDPSSDEA-IPTRFPPG---TVLPQGY-YI | | | | |
| Bovine corona NP | (153) | ADVNTPADIVDRDPSSDEA-IPTRFPPG---TVLPQGY-YI | | | | |
| avian infectious bronchitis virus NP | (121) | AVKSRSNQGT-PD-DKFDQY-LR-SDSGPDGNERWDFIP | | | | |
| mouse hepatitis virus NP | (156) | ADVNTPADIVDRDPSSDEA-IPTRFPPG---TVLPQGY-YI | | | | |
| Consensus | (157) | ADVNTPADIVDRDPSSDEA-IPTRFPPG TVLPQGY-YI | | | | |
| | | Section 6 | | | | |
| | | (196) | 196 | 210 | 220 | 234 |
| human coronavirus OC43 NP | (189) | EGSGRSAPNSRSTSRASSAGSRSRANS-NGNRTPTSG | | | | |
| Bovine corona NP | (189) | EGSGRSAPNSRSTSRASSAGSRSRANS-NGNRTPTSG | | | | |
| avian infectious bronchitis virus NP | (160) | LSRA-RRGRSTAASSAASSRVPSR-----EGSGRRREG | | | | |
| mouse hepatitis virus NP | (192) | EGSGRSAPNSRSTSRASSAGSRSRANS-NGNRTPTSG | | | | |
| Consensus | (196) | EGSGRSAPNSRSTSRASSAGSRSRANS-NGNRTPTSG | | | | |

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FIGURE 4B (contd.)

Section 7

| | (235) | 235 | 240 | 250 | 260 | 273 |
|--|-------|-----|-----|-------|------|-------------------------------|
| human coronavirus OC43 NP (228) | | VT | PD | MADQ | IASL | VLAKLGKDATKPPQOVTHHTAKIVRQKI |
| Bovine corona NP (228) | | VT | PD | MADQ | IASL | VLAKLGKDATKPPQOVTKQTAKETROKI |
| avian infectious bronchitis virus NP (192) | | AED | LI | ARAT | KII | QDQQ----RKGTRIIQK EEMAHRR |
| mouse hepatitis virus NP (229) | | VK | PI | MAEEI | AL | VLAKLGKDATGQPKQVTKOS K VROKI |
| Consensus (235) | | VT | PD | MADQ | IASL | VLAKLGKDATKPPQOVTKQTAKETVRQKI |

Section 8

| | (274) | 274 | 280 | 290 | 300 | 312 |
|--|-------|-----|-------|-----|--------|--------------------------|
| human coronavirus OC43 NP (267) | | LN | IPROK | SP | NKQCTV | QCCFKRGPNQ--HFGGEMLKL |
| Bovine corona NP (267) | | LN | KPROK | SP | NKQCTV | QCCFKRGPNQ--HFGGEMLKL |
| avian infectious bronchitis virus NP (227) | | FC | I---- | TV | PPGYR | LDVHCPRTKGKEGNEFDDKLNNEE |
| mouse hepatitis virus NP (268) | | LN | KPROK | TEN | KQCP | QCCFKRGPNQ--HFGGEMLKL |
| Consensus (274) | | LN | KPROK | RSP | NKQCTV | QCCFKRGPNQ NFGGEMLKL |

Section 9

| | (313) | 313 | 320 | 330 | 340 | 351 |
|--|-------|-----|-----|------|------|---------------------------|
| human coronavirus OC43 NP (304) | | GT | SD | QFP | ILAE | LAPTAGAFFGSRLELAKVQN----- |
| Bovine corona NP (304) | | GT | SD | QFP | ILAE | LAPTAGAFFGSRLELAKVQN----- |
| avian infectious bronchitis virus NP (262) | | GI | KD | GRVT | AMLN | ITSPHACLGRVTPKLQPDGLHLRF |
| mouse hepatitis virus NP (305) | | GT | SD | QFP | ILAE | LAPTAGAFFGSRLELAKVQN----- |
| Consensus (313) | | GT | SD | QFP | ILAE | LAPTAGAFFGSRLELAKVQN |

Section 10

| | (352) | 352 | 360 | 370 | 380 | 390 |
|--|-------|-----|-------|-------|-------|----------------------------|
| human coronavirus OC43 NP (337) | | --- | LS | GNPDE | OK | DVYELRYNGAIFRDSLSGFTIMKV |
| Bovine corona NP (337) | | --- | LS | GNLDE | OK | DVYELRYNGAIFRDSLSGFTIMKV |
| avian infectious bronchitis virus NP (301) | | EFT | TVVPR | DDQ | QFN | VKICDECVDGVGRPKDEVVRPK |
| mouse hepatitis virus NP (337) | | --- | SG | GADE | FTKDV | ELOYSGAVRDSLPGFETIMKV |
| Consensus (352) | | --- | LS | GN | DEP | QKDVYELRYNGAIFRDSLSGFTIMKV |

Section 11

| | (391) | 391 | 400 | 410 | 429 |
|--|-------|-----|------|------|----------------------------------|
| human coronavirus OC43 NP (373) | | LN | ENLN | AYQQ | QDGMMNMSPKPQORCHKNGO---GENDN |
| Bovine corona NP (373) | | LN | ENLN | AYQQ | QDGMMNMSPKPQORQKNGO---GENDN |
| avian infectious bronchitis virus NP (340) | | SR | PN | S--- | RPATRTSSPATRQCPQKKEKSKSK---KQDDE |
| mouse hepatitis virus NP (372) | | LN | ENLN | AYQ | KDGGADVVSFKPQI-KGRROAQEKKDEVND |
| Consensus (391) | | LN | ENLN | AYQQ | QDGMMNMSPKPQORQKNGO GENDN |

Section 12

| | (430) | 430 | 440 | 450 | 468 | |
|--|-------|-----|-----|--------|-------------------------------|-------------------------|
| human coronavirus OC43 NP (409) | | IS | VA | PKSRV | QQNKSRELTAEDISLLKKMDEP-----YT | |
| Bovine corona NP (409) | | IS | VA | APKSRV | QQNKSRELTAEDISLLKKMDEP-----YT | |
| avian infectious bronchitis virus NP (373) | | VD | K | LT | SDEERNI--AQTEFD | EPKVINWGDS-----A |
| mouse hepatitis virus NP (410) | | VS | V | KPKSS | VQRVSR | ELTPETRSLTAQTLDDGVVPDGL |
| Consensus (430) | | IS | VA | LPKSRV | QQNKSRELTAEDISLLKKMDDP | YT |

Section 13

| | (469) | 469 | 474 | |
|--|-------|-----|------|-----------------|
| human coronavirus OC43 NP (443) | | ED | TSEI | SEQ ID NO: 9915 |
| Bovine corona NP (443) | | ED | TSEI | SEQ ID NO: 9887 |
| avian infectious bronchitis virus NP (404) | | LG | ENEL | SEQ ID NO: 9906 |
| mouse hepatitis virus NP (449) | | ED | DSNV | SEQ ID NO: 9898 |
| Consensus (469) | | ED | TSEI | |

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FIGURE 4C

Section 1

| | (1) | 1 | 10 | 20 | 30 | 42 |
|---------------------------|-----|-----------|---------------------------------------|----|----|--------------|
| human coronavirus OC43 HE | (1) | ---- | MELLPRFILVSCIIGSLGIFY | P | T | NVSHVIGBLLFC |
| bovine coronavirus HE | (1) | ---- | MELLRLREVLVSCIIGSLGTDNP | P | T | NVSHLIGLNTFC |
| mouse hepatitis virus HE | (1) | MARTDAMAP | PTLLVLVSLGYAFGE | E | L | VSLINDLLEPC |
| Consensus | (1) | | MFLLPFILVSCIIGSLGFFNPPTNVVSHLNGDWFLFG | | | |

Section 2

| | (43) | 43 | 50 | 60 | 70 | 84 |
|---------------------------|------|----------------|-----------|-------------------|----|----|
| human coronavirus OC43 HE | (39) | DSRSDCNHIVNINP | NYSYMDLNP | LCDSGKISSKAGNSIFR | | |
| bovine coronavirus HE | (39) | DSRSDCNHIVNINP | NYSYMDLNP | LCDSGKISSKAGNSIFR | | |
| mouse hepatitis virus HE | (43) | DSRSDCNHIVNINP | NYSYMDLNP | LCDSGKISSKAGNSIFR | | |
| Consensus | (43) | DSRSDCNHIVNINP | NYSYMDLNP | LCDSGKISSKAGNSIFR | | |

Section 3

| | (85) | 85 | 90 | 100 | 110 | 126 |
|---------------------------|------|---------------|----------------------|-----|-----|---------|
| human coronavirus OC43 HE | (81) | SFHFTDFYNYTGE | GQQIIFYEGVNFTPYHAFKC | | | SGSNDIW |
| bovine coronavirus HE | (81) | SFHFTDFYNYTGE | GQQIIFYEGVNFTPYHAFKC | | | SGSNDIW |
| mouse hepatitis virus HE | (85) | SFHFTDFYNYTGE | GQQIIFYEGVNFTPYHAFKC | | | SGSNDIW |
| Consensus | (85) | SFHFTDFYNYTGE | GQQIIFYEGVNFTPYHAFKC | | | SGSNDIW |

Section 4

| | (127) | 127 | 140 | 150 | 168 |
|---------------------------|-------|---------------|----------------------------|-----|-----|
| human coronavirus OC43 HE | (123) | MONKGLFYTQVYK | NAVYRSLTFVNPVYNGSAQSTALCKS | | |
| bovine coronavirus HE | (123) | MONKGLFYTQVYK | NAVYRSLTFVNPVYNGSAQSTALCKS | | |
| mouse hepatitis virus HE | (127) | MONKGLFYTQVYK | NAVYRSLTFVNPVYNGSAQSTALCKS | | |
| Consensus | (127) | MONKGLFYTQVYK | NAVYRSLTFVNPVYNGSAQSTALCKS | | |

Section 5

| | (169) | 169 | 180 | 190 | 200 | 210 |
|---------------------------|-------|--------|-------------------|------|------|----------|
| human coronavirus OC43 HE | (165) | GS---- | LVLNTPAYIAPOANSGL | YTKV | ADYY | SGCDEYIV |
| bovine coronavirus HE | (165) | GS---- | LVLNTPAYIAPOANSGL | YTKV | ADYY | SGCDEYIV |
| mouse hepatitis virus HE | (169) | IANGVT | TLNTPAYIAPOANSGL | YTKV | ADYY | SGCDEYIV |
| Consensus | (169) | GS | LVLNTPAYIAPOANSGL | YTKV | ADYY | SGCDEYIV |

Section 6

| | (211) | 211 | 220 | 230 | 240 | 252 |
|---------------------------|-------|----------------|-----------------------------|-----|-----|-----|
| human coronavirus OC43 HE | (203) | PLCIFNGKFLSNTK | YDDSQYYFNKDTGVIYGLNSTETITTG | | | |
| bovine coronavirus HE | (203) | PLCIFNGKFLSNTK | YDDSQYYFNKDTGVIYGLNSTETITTG | | | |
| mouse hepatitis virus HE | (211) | PLCIFNGKFLSNTK | YDDSQYYFNKDTGVIYGLNSTETITTG | | | |
| Consensus | (211) | PLCIFNGKFLSNTK | YDDSQYYFNKDTGVIYGLNSTETITTG | | | |

Section 7

| | (253) | 253 | 260 | 270 | 280 | 294 |
|---------------------------|-------|---------------|-------------------------------|-----|-----|-----|
| human coronavirus OC43 HE | (245) | FDLNCHYLVLPSG | NYLAISNELLLTVPTKAICLNKRKDFTPV | | | |
| bovine coronavirus HE | (245) | FDLNCHYLVLPSG | NYLAISNELLLTVPTKAICLNKRKDFTPV | | | |
| mouse hepatitis virus HE | (253) | FDLNCHYLVLPSG | NYLAISNELLLTVPTKAICLNKRKDFTPV | | | |
| Consensus | (253) | FDLNCHYLVLPSG | NYLAISNELLLTVPTKAICLNKRKDFTPV | | | |

FIGURE 4C (contd.)

Section 8

| | (295) | 295 | 300 | 310 | 320 | 336 |
|---------------------------------|-------|------|--|-----|-----|-----|
| human coronavirus OC43 HE (287) | | QVVD | SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN | | | |
| bovine coronavirus HE (287) | | QVVD | SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN | | | |
| mouse hepatitis virus HE (295) | | QVVD | SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN | | | |
| Consensus (295) | | QVVD | SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN | | | |

Section 9

| | (337) | 337 | 350 | 360 | 378 |
|---------------------------------|-------|-------|---------------------------------------|-----|-----|
| human coronavirus OC43 HE (329) | | HGDAG | FTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR | | |
| bovine coronavirus HE (329) | | HGDAG | FTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR | | |
| mouse hepatitis virus HE (337) | | HGDAG | FTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR | | |
| Consensus (337) | | HGDAG | FTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR | | |

Section 10

| | (379) | 379 | 390 | 400 | 410 | 420 |
|---------------------------------|-------|------|---------------------------------------|-----|-----|-----|
| human coronavirus OC43 HE (371) | | CPTA | ADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY | | | |
| bovine coronavirus HE (371) | | CPTA | ADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY | | | |
| mouse hepatitis virus HE (379) | | CPTA | ADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY | | | |
| Consensus (379) | | CPTA | ADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY | | | |

Section 11

| | (421) | 421 | 432 | |
|---------------------------------|-------|--------|--------|-----------------|
| human coronavirus OC43 HE (413) | | FMVDNG | TRLHDA | SEQ ID NO: 9916 |
| bovine coronavirus HE (413) | | FMVDNG | TRLHDA | SEQ ID NO: 9888 |
| mouse hepatitis virus HE (420) | | FMVDNG | TRLHDA | SEQ ID NO: 9899 |
| Consensus (421) | | FMVDNG | TRLHDA | |

FIGURE 4D

Section 1

| | (1) | 1 | 10 | 20 | 39 |
|--------------------------------------|-----|----|-----------------------------------|----|---------|
| bovine coronavirus Sm | (1) | MF | MADAYFADTVWYVGQITFIVAICLLVII | -- | VVVAFLA |
| avian infectious bronchitis virus Sm | (1) | MN | LLNKSEENGSELTALYIIIVGFLATYLLGRALQ | -- | IVVAFLA |
| mouse hepatitis virus Sm | (1) | -- | MFNLEFLDTVWYVGQITFIVAICLLVII | -- | IVVAFLA |
| Consensus | (1) | M | M | N | FL |

Section 2

| | (40) | 40 | 50 | 60 | 78 |
|--------------------------------------|------|----|------------------|---------------------|------|
| bovine coronavirus Sm | (38) | TE | KLCIQLCGLCNTLVLS | SPSTYVFNNRGROFYEEYN | -DVK |
| avian infectious bronchitis virus Sm | (40) | AA | DAICLPWYTWVVI | PGAKGTAFVYKTYGRKLN | PEDE |
| mouse hepatitis virus Sm | (36) | SI | KLCIQLCGLCNTLVLS | SPSTYLYDRSKOLYKYNN | EEMR |
| Consensus | (40) | S | KLCIQLCGLCNTLVLS | PSIYLF | R |

Section 3

| | (79) | 79 | 90 | 108 | |
|--------------------------------------|------|----|------------------------------|-------|-----------------|
| bovine coronavirus Sm | (76) | PP | VLDVDDV | ----- | SEQ ID NO: 9889 |
| avian infectious bronchitis virus Sm | (79) | AV | IVNEFPKNGWNNKNPANFQDAQRDKLYS | ----- | SEQ ID NO: 9907 |
| mouse hepatitis virus Sm | (75) | LP | LELVDDI | ----- | SEQ ID NO: 9900 |
| Consensus | (79) | P | ILDVDDI | ----- | |

FIGURE 4E

| | | Section 1 | | | | |
|-------------------------------------|-------|-----------|---------|----------|------------|-----------------------|
| | | (1) | 1 | 10 | 20 | 30 40 |
| human coronavirus OC43 M | (1) | - | MSSKTTT | PAPVY | VIWTADEA | IKFLKEWNFSLGII |
| bovine coronavirus M | (1) | - | MSSVTTT | PAPVYT | WTADEA | IKFLKEWNFSLGII |
| avian infectious bronchitis virus M | (1) | - | ----- | MSNAANCT | LDCEOSVELF | LYNLETTATFL |
| mouse hepatitis virus M | (1) | MT | STTQAPQ | PPVYQW | TADFAIRPL | FWNESLGI |
| Consensus | (1) | MSS | TTT | PAPVYT | WTADEA | IKFLKEWNFSLGIILLFITII |
| | | Section 2 | | | | |
| | | (41) | 41 | 50 | 60 | 70 80 |
| human coronavirus OC43 M | (40) | LQFG | YTSRSM | FVYVIK | MIILWLM | WPLTII |
| bovine coronavirus M | (40) | LQFG | YTSRSM | FVYVIK | MIILWLM | WPLTII |
| avian infectious bronchitis virus M | (36) | LQYCL | ATSRREI | IMAV | CFWEN | IAMGVIS |
| mouse hepatitis virus M | (41) | LQFG | YTSRSM | FVYVIK | MIILWLM | WPLTII |
| Consensus | (41) | LQFG | YTSRSM | FVYVIK | MIILWLM | WPLTII |
| | | Section 3 | | | | |
| | | (81) | 81 | 90 | 100 | 110 120 |
| human coronavirus OC43 M | (80) | NVYL | GFSLV | PTIV | AIIMWIV | FVNSIRL |
| bovine coronavirus M | (80) | NVYL | GFSLV | PTIV | AIIMWIV | FVNSIRL |
| avian infectious bronchitis virus M | (76) | TGGH | VAAKIL | EVAC | LSFEGW | IO |
| mouse hepatitis virus M | (81) | NVYL | GFSLV | PTIV | AIIMWIV | FVNSIRL |
| Consensus | (81) | NVYL | GFSLV | PTIV | AIIMWIV | FVNSIRL |
| | | Section 4 | | | | |
| | | (121) | 121 | 130 | 140 | 150 160 |
| human coronavirus OC43 M | (120) | ETNN | LMCID | DMKGT | MYVRPI | IEDYHTLT |
| bovine coronavirus M | (120) | ETNN | LMCID | DMKGR | MYVRPI | IEDYHTLT |
| avian infectious bronchitis virus M | (116) | SN | AVGSL | LLSNG | QOCNFA | ESVPMVLS |
| mouse hepatitis virus M | (121) | ETNN | LMCID | DMKGT | MYVRPI | IEDYHTLT |
| Consensus | (121) | ETNN | LMCID | DMKGT | MYVRPI | IEDYHTLT |
| | | Section 5 | | | | |
| | | (161) | 161 | 170 | 180 | 190 200 |
| human coronavirus OC43 M | (160) | KLGT | GYSLSD | LPA | YVTVAKV | SHLCTYKR |
| bovine coronavirus M | (160) | KLGT | GYSLSD | LPA | YVTVAKV | SHLCTYKR |
| avian infectious bronchitis virus M | (156) | QWLAK | CEPDH | PKDIF | CPPDR | RNI |
| mouse hepatitis virus M | (161) | KLGT | GYSLSD | LPA | YVTVAKV | SHLCTYKR |
| Consensus | (161) | KLGT | GYSLSD | LPA | YVTVAKV | SHLCTYKR |
| | | Section 6 | | | | |
| | | (201) | 201 | 210 | 220 | 231 |
| human coronavirus OC43 M | (200) | AVYV | KSKV | GN | YRLP | STQKGS |
| bovine coronavirus M | (200) | AVYV | KSKV | GN | YRLP | STQKGS |
| avian infectious bronchitis virus M | (185) | QK | YTG | DQSE | NKKRF | AT |
| mouse hepatitis virus M | (201) | AVYV | KSKV | GN | YRLP | SN |
| Consensus | (201) | AVYV | KSKV | GN | YRLP | STQKGS |

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 SEQ ID NO: 9890
 SEQ ID NO: 9908
 SEQ ID NO: 9901

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FIGURE 4F

| | | Section 1 | | | | |
|---------------------------------|-------|---------------|---------------|------------|----------|--------------------|
| | | (1) | 1 | 10 | 20 | 30 |
| human coronavirus OC43 S | (1) | MFLILLISLPTAF | AVIGDLKCTSDN | INDKDTGPP | PPI | ISTD |
| avianinfectiousbronchitisvirusS | (1) | ----- | | | | |
| bovine coronavirus S | (1) | MFLILLISLPTAF | AVIGDLKCTTVS | INDVDTGVP | PST | STD |
| mouse hepatitis virus S | (1) | MLFMFLFLP | SCLCGYIGDFRCI | QLVNSNGANV | SAP | SISTE |
| Consensus | (1) | MFLILLISLPTAF | AVIGDLKCTSL | IND | DTG | PSISTD |
| | | Section 2 | | | | |
| | | (41) | 41 | 50 | 60 | 70 |
| human coronavirus OC43 S | (40) | TVDVTNGLGTY | YVLDRVYINT | LLFNGYYPTS | SGSTYR | NMA |
| avianinfectiousbronchitisvirusS | (1) | ----- | MLV | PLILVTLL | CALCSA | VLYD |
| bovine coronavirus S | (40) | TVDVTNGLGTY | YVLDRVYINT | LLFNGYYPTS | SGSTYR | NMA |
| mouse hepatitis virus S | (41) | TVEVSQGLGTY | YVLDRVYLNAT | LLLTGYY | PVDGSK | FENLA |
| Consensus | (41) | TVDVTNGLGTY | YVLDRVYLN | TTLLNGYY | PTSGSTYR | NMA |
| | | Section 3 | | | | |
| | | (81) | 81 | 90 | 100 | 110 |
| human coronavirus OC43 S | (80) | LKGSVLHSRL | WKPFELSDEIN | GIFAKV | KNTKVIK | DRVMY |
| avianinfectiousbronchitisvirusS | (23) | SSSYVYYYQ | SAFRITSGWH | LOGAYAV | NISSEFN | NAGSS |
| bovine coronavirus S | (80) | LKGTLLLS | TLWEKEEFL | SDFTN | IPAK | KNTKVEK |
| mouse hepatitis virus S | (81) | ETGTNSV | SLSWFOQ | YLSQFND | IFAK | ONLKTST |
| Consensus | (81) | LKGTVLLS | SWFKPPFL | SDFNNGI | EFAK | VKNTKVIK |
| | | Section 4 | | | | |
| | | (121) | 121 | 130 | 140 | 150 |
| human coronavirus OC43 S | (120) | SEFPATITG | SFTVNTSY | SVVVQ | PR | TINST |
| avianinfectiousbronchitisvirusS | (63) | SGCTVGI | THGGRV | NASSI | AMTAP | -----S----- |
| bovine coronavirus S | (120) | SEFPATITG | SFTVNTSY | SVVVQ | PR | -----HTTILGNKIQGFL |
| mouse hepatitis virus S | (121) | AYEPTTIV | EGSLEGY | TSYTV | VIEP | -----YNG-----VI |
| Consensus | (121) | SEFPATITG | SFTVNTSY | SVVVQ | P | TGNKLQGLL |
| | | Section 5 | | | | |
| | | (161) | 161 | 170 | 180 | 190 |
| human coronavirus OC43 S | (160) | EVSVCQY | NMCEYP | QTTCHPN | LG-NHR | KELWH |
| avianinfectiousbronchitisvirusS | (88) | ---GMA | WSSSQ | FCTAH | NFS | DTTVE |
| bovine coronavirus S | (156) | ETVCO | YTMCE | YPNTI | CNP | NLG-NOR |
| mouse hepatitis virus S | (149) | MASVCQ | YTLCL | LPYTD | CKPNT | NGNKLIG |
| Consensus | (161) | EISVCQ | YTMCE | YPNTIC | NPNLG | NRIELWH |
| | | Section 6 | | | | |
| | | (201) | 201 | 210 | 220 | 230 |
| human coronavirus OC43 S | (199) | YKRNF | TYDVN | ADYLY | FHFYQ | EGGTFY |
| avianinfectiousbronchitisvirusS | (126) | LQQLIR | VSAMK | NGQLF | YNLTV | SVAKY |
| bovine coronavirus S | (195) | YKRNF | TYDVN | ADYLY | FHFYQ | EGGTFY |
| mouse hepatitis virus S | (189) | LKRNF | TLNVN | ADAFY | TFHFYQ | HGGTFY |
| Consensus | (201) | YKRNF | TYDVN | ADYLY | FHFYQ | EGGTFY |

FIGURE 4F (contd.)

| Section 7 | | | | | | |
|---------------------------------|-------|--|---------------------------|-----|------------------|-----|
| | (241) | 241 | 250 | 260 | 270 | 280 |
| human coronavirus OC43 S | (239) | NYVLEGMALSHYYVMPITCN---- | SKLTLEYWVTPLTSTROY | | | |
| avianinfectiousbronchitisvirusS | (166) | SYVLENGDLYVTSNETLDVTSAGVYFKAGGPITYKVMREVK | | | | |
| bovine coronavirus S | (235) | NYVLEGTMLSHYYVMBLTCN---- | SALTLEYWVTPLTSTROY | | | |
| mouse hepatitis virus S | (229) | SYVLEGTMLSHYYVMBLTCN---- | SALTLEYWVTPLTSTROY | | | |
| Consensus | (241) | SVYLG | ILSHYYVMPITCN | A S | LTLEYWVTPLTSTROY | |
| Section 8 | | | | | | |
| | (281) | 281 | 290 | 300 | 310 | 320 |
| human coronavirus OC43 S | (275) | LLAFNODLITFNAED | MSDEMSEIKCKTQSIAPPTGVYEL | | | |
| avianinfectiousbronchitisvirusS | (206) | ALAYFVNGTAQDVIL | DCSPRGLLACQYNTGNFSDQFLPF | | | |
| bovine coronavirus S | (271) | LLAFNODLITFNAED | MSDEMSEIKCKTQSIAPPTGVYEL | | | |
| mouse hepatitis virus S | (269) | LFNENQKLVITSAVD | CASSYTSEIKCKTQSMPLSTGVYEL | | | |
| Consensus | (281) | LLAFNQDGVIFNAVDC | SSFMSSEIKCKTQSIAPSTGVYEL | | | |
| Section 9 | | | | | | |
| | (321) | 321 | 330 | 340 | 350 | 360 |
| human coronavirus OC43 S | (315) | NGYTVQPIADVYRRKPNLENCNLEAWLNDRKSVPSPLNWER | | | | |
| avianinfectiousbronchitisvirusS | (246) | TNSSLVKQKFEVYK----- | ENSVNTTCTLHNFIENH | | | |
| bovine coronavirus S | (311) | NGYTVQPIADVYRRKPNLENCNLEAWLNDRKSVPSPLNWER | | | | |
| mouse hepatitis virus S | (309) | SGYTVQPVGVVYRRVANLPACNLEAWLNDRKSVPSPLNWER | | | | |
| Consensus | (321) | NGYTVQPIADVYRRIPNLP | CNIEAWLNDRKSVPSPLNWER | | | |
| Section 10 | | | | | | |
| | (361) | 361 | 370 | 380 | 390 | 400 |
| human coronavirus OC43 S | (355) | KTFESNCNFMMSSTMSFIQADSFCTCNNIDAAKIYGMCFSSI | | | | |
| avianinfectiousbronchitisvirusS | (277) | ETGALPNP----- | SGVNIQTYQTKTAQSGYINFN | SFL | | |
| bovine coronavirus S | (351) | KTFESNCNFMMSSTMSFIQADSFCTCNNIDAAKIYGMCFSSI | | | | |
| mouse hepatitis virus S | (349) | KTFESNCNFMMSSTMSFIQADSFCTCNNIDAASKV | GRCFGST | | | |
| Consensus | (361) | KTFESNCNFMMSSTMSFIQADSFCTCNNIDAAKIYGMCFSSI | | | | |
| Section 11 | | | | | | |
| | (401) | 401 | 410 | 420 | 430 | 440 |
| human coronavirus OC43 S | (395) | TIDKFAIPNGRKVDLQGLNIGYLOSEFNRYRIDTTATSCQLY | | | | |
| avianinfectiousbronchitisvirusS | (311) | SSFVYKESNEMYGSYHPSCKFRLETIANGLWFNSLSVSTIA | | | | |
| bovine coronavirus S | (391) | TIDKFAIPNGRKVDLQGLNIGYLOSEFNRYRIDTTATSCQLY | | | | |
| mouse hepatitis virus S | (389) | SVDKFAVPRSRQVDLQGLNSGFLQATANYRIDTAATSCQLH | | | | |
| Consensus | (401) | SIDKFAIPNGRKVDLQGLNIGYLOSEFNRYRIDTTATSCQLY | | | | |
| Section 12 | | | | | | |
| | (441) | 441 | 450 | 460 | 470 | 480 |
| human coronavirus OC43 S | (435) | YNLPAANVSVSRFPSTWNKRFGFIEDSVFKERPAGVLTN | | | | |
| avianinfectiousbronchitisvirusS | (351) | YGP----- | LQG----- | | | |
| bovine coronavirus S | (431) | YNLPAANVSVSRFPSTWNKRFGFIEDSVFKERPAGVLTN | | | | |
| mouse hepatitis virus S | (429) | YTLPKNNVTINNHNPSWNNRRYGFENDAGVEGKN----- | Q | | | |
| Consensus | (441) | YNLPAANVSVSRFPSTWNKRFGF | E SVFKERPAGV | TN | | |

FIGURE 4F (contd.)

| | | | | | | Section 13 |
|---------------------------------|-------|-------------------|------------------------|----------|-------------|------------------|
| | (481) | 481 | 490 | 500 | 510 | 520 |
| human coronavirus OC43 S | (475) | HDVVYAQHCFKAPKNF | EPCKING | -SCVGS | GP----- | GKNN |
| avianinfectiousbronchitisvirusS | (357) | ---GCKQSVFKGRATC | YAYS | YGGPS | ICKGV | YSG----- |
| bovine coronavirus S | (471) | HDVVYAQHCFKASTNF | CPCKLDGSL | CVGN | GGEG | GIDAGYKTS |
| mouse hepatitis virus S | (463) | HDVVYAQCCETVRSSYP | CAQPDIV | SPCTT | QTK----- | P |
| Consensus | (481) | HDVVYAQHCFKARSNFC | PKCL | G | LSVGS | GP K |
| | | | | | | Section 14 |
| | (521) | 521 | 530 | 540 | 550 | 560 |
| human coronavirus OC43 S | (509) | GIGTCPAGTNYLT | CDN----- | LC | TRDPIT-- | FTGT |
| avianinfectiousbronchitisvirusS | (388) | ----- | ----- | ----- | ----- | ----- |
| bovine coronavirus S | (511) | GIGTCPAGTNYLT | CHNAAQC | DC | LC | TPDELT |
| mouse hepatitis virus S | (497) | ----- | ----- | ----- | ----- | ----- |
| Consensus | (521) | GIGTCPAGTNYLT | C N | | LC | TPDPIT TG YKCP |
| | | | | | | Section 15 |
| | (561) | 561 | 570 | 580 | 590 | 600 |
| human coronavirus OC43 S | (541) | QTKSLVGIGEH | SGLAVKSDYC | ----- | GNS | QTCR |
| avianinfectiousbronchitisvirusS | (388) | ---ELDHNFE | GLIVYVTKSG | ----- | ----- | ----- |
| bovine coronavirus S | (551) | QTKYLVGIGEH | SGLAIKSDHC | ----- | GNP | CTCQ |
| mouse hepatitis virus S | (497) | -KSAFVN | VGDHCEGIGVLEDNC | G | NADPHKGC | ICANNSEIG |
| Consensus | (561) | QTKALVGIGEHCS | GGLAVKSDHCG | | GN | CTC PQAFLG |
| | | | | | | Section 16 |
| | (601) | 601 | 610 | 620 | 630 | 640 |
| human coronavirus OC43 S | (577) | WSADSC | LOGDKCNIFANFIL | HDVNSGLT | CSTD | L KANTDI |
| avianinfectiousbronchitisvirusS | (407) | ----- | ----- | SR- | IQ | ATEPEPVITONHYNEL |
| bovine coronavirus S | (587) | WSVDS | CLOGDRCNIFANFIL | HDVNSGLT | CSTD | L KSNITDI |
| mouse hepatitis virus S | (536) | WSHDT | GLVNDRCQIFANILL | NCINS | GGTTC | STD |
| Consensus | (601) | WS | DSCLOGDRCNIFANFIL | HDINS | GGTTC | STD LQKANTDI |
| | | | | | | Section 17 |
| | (641) | 641 | 650 | 660 | 670 | 680 |
| human coronavirus OC43 S | (617) | ILGVCVN | DLGIL | GGIFVE | NATYYNS | WQNL |
| avianinfectiousbronchitisvirusS | (427) | TLNTQ | DNITGRTG | CFITN | TD | SAVS-- |
| bovine coronavirus S | (627) | ILGVCVN | DLGIL | GGIFVE | NATYYNS | WQNL |
| mouse hepatitis virus S | (576) | VTGL | SVKNDLYCIT | GGVFE | KADYYNS | WQTL |
| Consensus | (641) | ILGVCVN | YDLYGIT | GQGI | FVEVNATYYNS | WQNL |
| | | | | | | Section 18 |
| | (681) | 681 | 690 | 700 | 710 | 720 |
| human coronavirus OC43 S | (657) | LYGFRDY | ITNRTFMIRSCYSGRV | SAAFHANS | SSEP | ALLFRN |
| avianinfectiousbronchitisvirusS | (465) | ILD | TSGSIDIFVVQGEYGLNYYKVN | PCEDVN | QQFV | VSGGK |
| bovine coronavirus S | (667) | LYGFRDY | LTNRTFMIRSCYSGRV | SAAFHANS | SSEP | ALLFRN |
| mouse hepatitis virus S | (616) | LNGFRD | LTNKTYTIRSCYSGRV | SAAH | KDA | PEPALLYRN |
| Consensus | (681) | LYGFRDY | ITNRTFMIRSCYSGRV | SAAFHANS | SSEP | ALLFRN |

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FIGURE 4F (contd.)

| Section 19 | | | | | |
|---------------------------------|-------|---|-----|-----|---------|
| | (721) | 721 | 730 | 740 | 750 760 |
| human coronavirus OC43 S | (697) | IKCNYVFNNLSITRQLQPINYFDSYLGCVVNAYNSTAISVQ | | | |
| avianinfectiousbronchitisvirusS | (505) | LVGILTSTRNETGSOELLENOFYIKITNGTRRRFRRSITENVA | | | |
| bovine coronavirus S | (707) | IKCNYVFNNILSRQLQPINYFDSYLGCVVNADNSTSSVVO | | | |
| mouse hepatitis virus S | (656) | INGSYVESINISREENPLNYFDSYLGCVVNADNRTDEALP | | | |
| Consensus | (721) | IKCNYVFNNLSLRQLQPINYFDSYLGCVVNADNSTSEAVQ | | | |
| Section 20 | | | | | |
| | (761) | 761 | 770 | 780 | 790 800 |
| human coronavirus OC43 S | (737) | TCDLTVGSGYCVDYSKNRRSRGAIPTGYRFTNFEFFTUNS | | | |
| avianinfectiousbronchitisvirusS | (545) | NCPYVSYGKEQIKPDG-----SIATIVPKQL | | | |
| bovine coronavirus S | (747) | TCDLTVGSGYCVDYSTKRRSRRSITTTGYRFTNFEFFTUNS | | | |
| mouse hepatitis virus S | (696) | NQDLRMGAGLEVDYSKSRRADRSVSTGYRLTTFEFTPML | | | |
| Consensus | (761) | TCDLTVGSGYCVDYSK RRSRRSITTTGYRFTNFEFFTUNS | | | |
| Section 21 | | | | | |
| | (801) | 801 | 810 | 820 | 830 840 |
| human coronavirus OC43 S | (777) | VNDSLEPVGGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDC | | | |
| avianinfectiousbronchitisvirusS | (571) | EQFVAPLFNVNTENVLLTENSENLTVTDYTFRMDVQINQ | | | |
| bovine coronavirus S | (787) | VNDSLEPVGGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDC | | | |
| mouse hepatitis virus S | (736) | VNDSVQSVVDGLYEMOITFTNTIGHHEEFLIRSPVTIDC | | | |
| Consensus | (801) | VNDSLEPVGGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDC | | | |
| Section 22 | | | | | |
| | (841) | 841 | 850 | 860 | 870 880 |
| human coronavirus OC43 S | (817) | AAFVCGDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ | | | |
| avianinfectiousbronchitisvirusS | (611) | LQYVCGSSLDNRKLFQQSGPVCDNILSVVNSGQKEEMEL | | | |
| bovine coronavirus S | (827) | AAFVCGDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ | | | |
| mouse hepatitis virus S | (776) | AAFVCGDNTACROOLVEYGSFCDNINAILTEVNELLDMO | | | |
| Consensus | (841) | AAFVCGDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ | | | |
| Section 23 | | | | | |
| | (881) | 881 | 890 | 900 | 910 920 |
| human coronavirus OC43 S | (857) | LQVANSIMNGVTTLSTKLKDGVNENVDIDNFSFVLGCLGSE | | | |
| avianinfectiousbronchitisvirusS | (651) | LNFYSSTKP-----AGENTPVLSNVSTGEFNISILLTNPS | | | |
| bovine coronavirus S | (867) | LQVANSIMNGVTTLSTKLKDGVNENVDIDNFSFVLGCLGSD | | | |
| mouse hepatitis virus S | (816) | LQVASALMOGVTLSSRLPDGTSGLPDDINFSPLIGCIGST | | | |
| Consensus | (881) | LQVASSIMNGVTTLSTKLKDGVNENVDIDNFSFVLGCLGSS | | | |
| Section 24 | | | | | |
| | (921) | 921 | 930 | 940 | 950 960 |
| human coronavirus OC43 S | (897) | CSKASS-----RSAIEDLLFDKVKLSDVGFVEAYNNCT | | | |
| avianinfectiousbronchitisvirusS | (686) | SRRKRS-----LTEDLEETSVEESVGLPTNDAYKNCF | | | |
| bovine coronavirus S | (907) | CNKVSS-----RSAIEDLLFDKVKLSDVGFVEAYNNCT | | | |
| mouse hepatitis virus S | (856) | CAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCT | | | |
| Consensus | (921) | CAK SS RSAIEDLLFDKVKLSDVGFVEAYNNCT | | | |

FIGURE 4F (contd.)

| Section 25 | | | | | | |
|---------------------------------|--------|--|------------------------------------|-----------------------|----------|------|
| | (961) | 961 | 970 | 980 | 990 | 1000 |
| human coronavirus OC43 S | (930) | GGAE-- | IRDLICVQSYKGIK | IRDLISENQISGYTLAATS | | |
| avianinfectiousbronchitisvirusS | (717) | AGPLGFFKCIACAREYN | LLALEETITAEMQALYTSSLVA | | | |
| bovine coronavirus S | (940) | GGAE-- | IRDLICVQSYN | IRDLISENQISGYTLAATS | | |
| mouse hepatitis virus S | (896) | GGQE-- | VRDLICVQSFNSIK | IRDLVLSQSQISGYTLTGATA | | |
| Consensus | (961) | GGAE | IRDLICVQSYNGIKVLPPLISENQISGYTLAATA | | | |
| Section 26 | | | | | | |
| | (1001) | 1001 | 1010 | 1020 | 1030 | 1040 |
| human coronavirus OC43 S | (968) | ASLFPFWT | AGVYFLNVQYR | INGLGVMDVLSQ | NQKLI | |
| avianinfectiousbronchitisvirusS | (757) | SMAAGGIT | AGATPATOLQAR | INHLGILQSLLELKNQEK | | |
| bovine coronavirus S | (978) | ASLFPWS | AGVYFLNVQYR | INGLGVMDVLSQ | NQKLI | |
| mouse hepatitis virus S | (934) | AAMFPWS | AGVYFLSVQYR | INGLGVMDVLSQ | NQKLI | |
| Consensus | (1001) | ASLFPWS | AAGVYFLNVQYR | INGLGVMDVLSQ | NQKLI | |
| Section 27 | | | | | | |
| | (1041) | 1041 | 1050 | 1060 | 1070 | 1080 |
| human coronavirus OC43 S | (1008) | ANAFNNALYAT | EGGFDATNSALVKIQAVVNANAEALNNLL | | | |
| avianinfectiousbronchitisvirusS | (797) | AASTNKAIGHM | EGGERSSLAQQTQD | VSKQSAILTETM | | |
| bovine coronavirus S | (1018) | ANAFNNALGATQEG | FDATNSALVKIQAVVNANAEALNNLL | | | |
| mouse hepatitis virus S | (974) | ASAFNNALGATQEG | FDATNSALGKIQSVVNANAEALNNLL | | | |
| Consensus | (1041) | ANAFNNALGAIQEG | FDATNSALVKIQAVVNANAEALNNLL | | | |
| Section 28 | | | | | | |
| | (1081) | 1081 | 1090 | 1100 | 1110 | 1120 |
| human coronavirus OC43 S | (1048) | QQLSNRFGAISASLQ | EILSRLEDALEANAQIDRLINGRLTA | | | |
| avianinfectiousbronchitisvirusS | (837) | ASTNKNFGAL | SVTQTYQQFD | TCQNVQVRLATGRSS | | |
| bovine coronavirus S | (1058) | QQLSNRFGAISASLQ | EILSRLEDALEANAQIDRLINGRLTA | | | |
| mouse hepatitis virus S | (1014) | NQLSNRFGAISASLQ | EILSRLEDALEANAQIDRLINGRLTA | | | |
| Consensus | (1081) | QQLSNRFGAISASLQ | EILSRLEDALEANAQIDRLINGRLTA | | | |
| Section 29 | | | | | | |
| | (1121) | 1121 | 1130 | 1140 | 1150 | 1160 |
| human coronavirus OC43 S | (1088) | LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC | | | | |
| avianinfectiousbronchitisvirusS | (877) | LSVLASAKQAEYIRVSQOREL | ATQREAFATISQIRYST | | | |
| bovine coronavirus S | (1098) | LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC | | | | |
| mouse hepatitis virus S | (1054) | LNAYLEKQLSDSTLVKFSAAQATELVNECVKSSSRINFC | | | | |
| Consensus | (1121) | LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC | | | | |
| Section 30 | | | | | | |
| | (1161) | 1161 | 1170 | 1180 | 1190 | 1200 |
| human coronavirus OC43 S | (1128) | GACNHIISLVQNAPYGLYFIHFSYVPTSFVTAKVSPGLCI | | | | |
| avianinfectiousbronchitisvirusS | (917) | GNGRAVLTIP | GNFNGIVPHFS | TDSEFVNVT | AIIVGFCV | |
| bovine coronavirus S | (1138) | GACNHIISLVQNAPYGLYFIHFSYVPTSFVTAKVSPGLCI | | | | |
| mouse hepatitis virus S | (1094) | GACNHIISLVQNAPYGLYFIHFSYVPTSFVTAKVSPGLCI | | | | |
| Consensus | (1161) | GACNHIISLVQNAPYGLYFIHFSYVPTSFVTAKVSPGLCI | | | | |

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FIGURE 4F (contd.)

| | | | | | | Section 31 |
|--|--------------|----------|-----------|-------------------|---------------|---------------|
| | (1201) | 1201 | 1210 | 1220 | 1230 | 1240 |
| human coronavirus OC43 S (1168) | AGDRG | ----- | L | PKS | YFVNVNNTWMY | IGSGYTYEPEPT |
| avianinfectiousbronchitisvirusS (957) | KPANASQYAI | VPANGR | ITIQVNGSY | YITARDM | M | RA |
| bovine coronavirus S (1178) | AGDRG | ----- | L | PKS | YFVNVNNTWMF | IGSGYTYEPEPT |
| mouse hepatitis virus S (1134) | SGDRG | ----- | L | PKA | YFVQDDGEK | FTGSSYTYEPEPT |
| Consensus (1201) | AGDRG | | | IAPKSGYFVNVNNTWMT | GTGSGYTYEPEPT | |
| | | | | | | Section 32 |
| | (1241) | 1241 | 1250 | 1260 | 1270 | 1280 |
| human coronavirus OC43 S (1202) | ENNVVVMSTCAV | NYTKAPYV | MLNTSIP | -NLPD | KE | LDQ |
| avianinfectiousbronchitisvirusS (997) | AGDV | TLTSEQAN | GVSVNKT | VITTFVDNDD | DFD | IND |
| bovine coronavirus S (1212) | ENNVVVMSTCAV | NYTKAPDV | MLNISTP | -NLPY | KE | LDQ |
| mouse hepatitis virus S (1168) | DKNS | VIMSSCAV | NYTKAREV | MLNTSIP | -NPPD | KE |
| Consensus (1241) | ENNVVVMSSCAV | NYTKAPDV | MLNTSIP | | NLPDFKE | ELDQW |
| | | | | | | Section 33 |
| | (1281) | 1281 | 1290 | 1300 | 1310 | 1320 |
| human coronavirus OC43 S (1241) | EKNQTSVAP | DLSDY | --TN | TF | ELQVEM | NLEA |
| avianinfectiousbronchitisvirusS (1037) | WNDTKHEL | DFDKFN | --YT | PI | LDSD | ID |
| bovine coronavirus S (1251) | EKNQTSVAP | DLSDY | --TN | TF | ELQVEM | NLEA |
| mouse hepatitis virus S (1207) | EKNQTSVAP | DLSDY | --TN | TF | ELQVEM | NLEA |
| Consensus (1281) | EKNQTSVAP | DLSDY | | INVTFLD | LQ | EMNRIQEA |
| | | | | | | Section 34 |
| | (1321) | 1321 | 1330 | 1340 | 1350 | 1360 |
| human coronavirus OC43 S (1279) | QSYINLKD | IGTYEY | VVWVW | LLIGL | AGVAM | LVLFFFI |
| avianinfectiousbronchitisvirusS (1075) | QSYINLKD | IGTYEY | VVWVW | LLIGL | AGVAM | LVLFFFI |
| bovine coronavirus S (1289) | QSYINLKD | IGTYEY | VVWVW | LLIGL | AGVAM | LVLFFFI |
| mouse hepatitis virus S (1247) | QSYINLKD | IGTYEY | VVWVW | LLIGL | AGVAM | LVLFFFI |
| Consensus (1321) | QSYINLKD | IGTYEY | VVWVW | LLIGL | AGVAM | LVLFFFI |
| | | | | | | Section 35 |
| | (1361) | 1361 | 1370 | 1380 | 1390 | 1400 |
| human coronavirus OC43 S (1319) | CCCTGCG | ----- | TSCFK | CGGCCDD | YTG | QELVIKT |
| avianinfectiousbronchitisvirusS (1115) | FFM | CGCGCCG | CGFIMPLMS | CGKKSS | YITFD | NDVVTE |
| bovine coronavirus S (1329) | CCCTGCG | ----- | TSCFK | CGGCCDD | YTG | QELVIKT |
| mouse hepatitis virus S (1287) | CCCTGCG | ----- | TSCFK | CGGCCDD | YTG | QELVIKT |
| Consensus (1361) | CCCTGCG | | | TSCFKKCGGCCDD | YTG | QELVIKT |
| | | | | | | Section 36 |
| | (1401) | 1401 | 1408 | | | |
| human coronavirus OC43 S (1350) | SHDD | ---- | | SEQ | ID NO: | 9918 |
| avianinfectiousbronchitisvirusS (1155) | QYRPKKS | V | | SEQ | ID NO: | 9909 |
| bovine coronavirus S (1360) | SHED | ---- | | SEQ | ID NO: | 9891 |
| mouse hepatitis virus S (1318) | NISSHED | - | | SEQ | ID NO: | 9902 |
| Consensus (1401) | SHDD | | | | | |

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FIGURE 5

| | | | | | | |
|-----------------------------|-------|---|-----|-----------------|-----|-----|
| | | Section 15 | | | | |
| | (589) | 589 | 600 | 610 | 620 | 630 |
| human coronavirus OC43 S | (565) | NS T R P Q A I L G V A D S C L Q G K C N I F A N F I L H D V N S G L T T C S | | | | |
| bovine coronavirus S | (575) | NP C T G Q P Q A F L G V S V D S C L Q G R C N I F A N F I L H D V A E T T C S | | | | |
| mouse hepatitis virus A59 S | (524) | K G I C A N N S I L G T C H D T C I V N R Q I L A N I L N G I T S G T T C S | | | | |
| Consensus | (589) | N C T C P Q A F L G W S D S C L Q G D R C N I F A N F I L H D V N S G T T C S | | | | |
| | | Section 16 | | | | |
| | (631) | 631 | 640 | 650 | 660 | 672 |
| human coronavirus OC43 S | (607) | T D L Q K A N T D I I L G V C V N Y D L Y G I T G Q G I F V E V N A T Y Y N S W Q N | | | | |
| bovine coronavirus S | (617) | T D L Q K S N I D T I L G V G N E E L G L T G Y I T V V N A T E R N G V N | | | | |
| mouse hepatitis virus A59 S | (566) | T D L I L E N T E V V T I L K Y H L G T T R G G V I K E V K A D L N S W I T | | | | |
| Consensus | (631) | T D L Q K A N T D I I L G V C V N Y D L Y G I T G Q G I F V E V N A T Y Y N S W Q N | | | | |
| | | Section 17 | | | | |
| | (673) | 673 | 680 | 690 | 700 | 714 |
| human coronavirus OC43 S | (649) | L L Y D S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P | | | | |
| bovine coronavirus S | (659) | L L Y D S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P | | | | |
| mouse hepatitis virus A59 S | (608) | L L Y D V S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P | | | | |
| Consensus | (673) | L L Y D S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P | | | | |
| | | Section 18 | | | | |
| | (715) | 715 | 720 | 730 | 740 | 756 |
| human coronavirus OC43 S | (691) | A L L F R N I K C N Y V F N N S L S R Q L P I N Y F D S Y L G C V V N A D N S T A | | | | |
| bovine coronavirus S | (701) | A L L F R N I K C N Y V F N N S L S R Q L P I N Y F D S Y L G C V V N A D N S T A | | | | |
| mouse hepatitis virus A59 S | (650) | A L L Y F R N I N G S Y V F S N I S T E E N C L N G C S Y L G C A V N A D N R T D | | | | |
| Consensus | (715) | A L L F R N I K C N Y V F N N S L S R Q L P I N Y F D S Y L G C V V N A D N S T A | | | | |
| | | Section 19 | | | | |
| | (757) | 757 | 770 | S1 ← 780 ↓ → S2 | | 798 |
| human coronavirus OC43 S | (733) | I S V Q T C D L T V G S G Y C V D Y S K N R R S R S I T T G Y R F T N F E P F T V | | | | |
| bovine coronavirus S | (743) | S V V Q T C D L T V G S G Y C V D Y S K N R R S R S I T T G Y R F T N F E P F T V | | | | |
| mouse hepatitis virus A59 S | (692) | E A L P N G D L R M C A L G V D Y S K S P H A H R S V S T G A L T T E L L Y P | | | | |
| Consensus | (757) | A V Q T C D L T V G S G Y C V D Y S K R R S R S I T T G Y R F T N F E P F T V | | | | |
| | | Section 20 | | | | |
| | (799) | 799 | 810 | 820 | 830 | 840 |
| human coronavirus OC43 S | (775) | N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C | | | | |
| bovine coronavirus S | (785) | N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C | | | | |
| mouse hepatitis virus A59 S | (734) | M L Y N D S V Q S M D C L L M D L P T N L I G H H E L L I S T R S S Y T I L L | | | | |
| Consensus | (799) | N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C | | | | |
| | | Section 21 | | | | |
| | (841) | 841 | 850 | 860 | 870 | 882 |
| human coronavirus OC43 S | (817) | A A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q | | | | |
| bovine coronavirus S | (827) | S A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q | | | | |
| mouse hepatitis virus A59 S | (776) | A A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q | | | | |
| Consensus | (841) | A A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q | | | | |

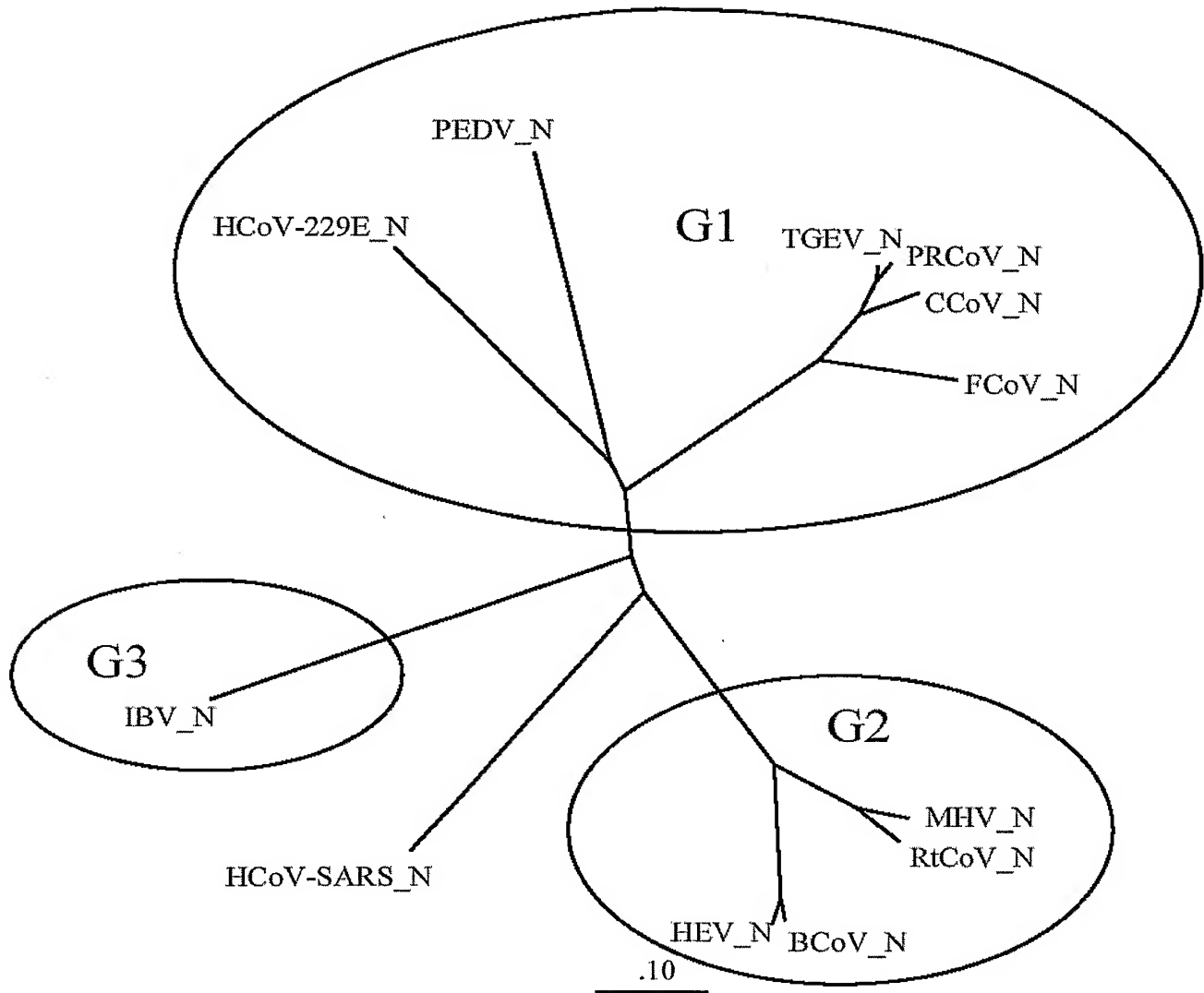
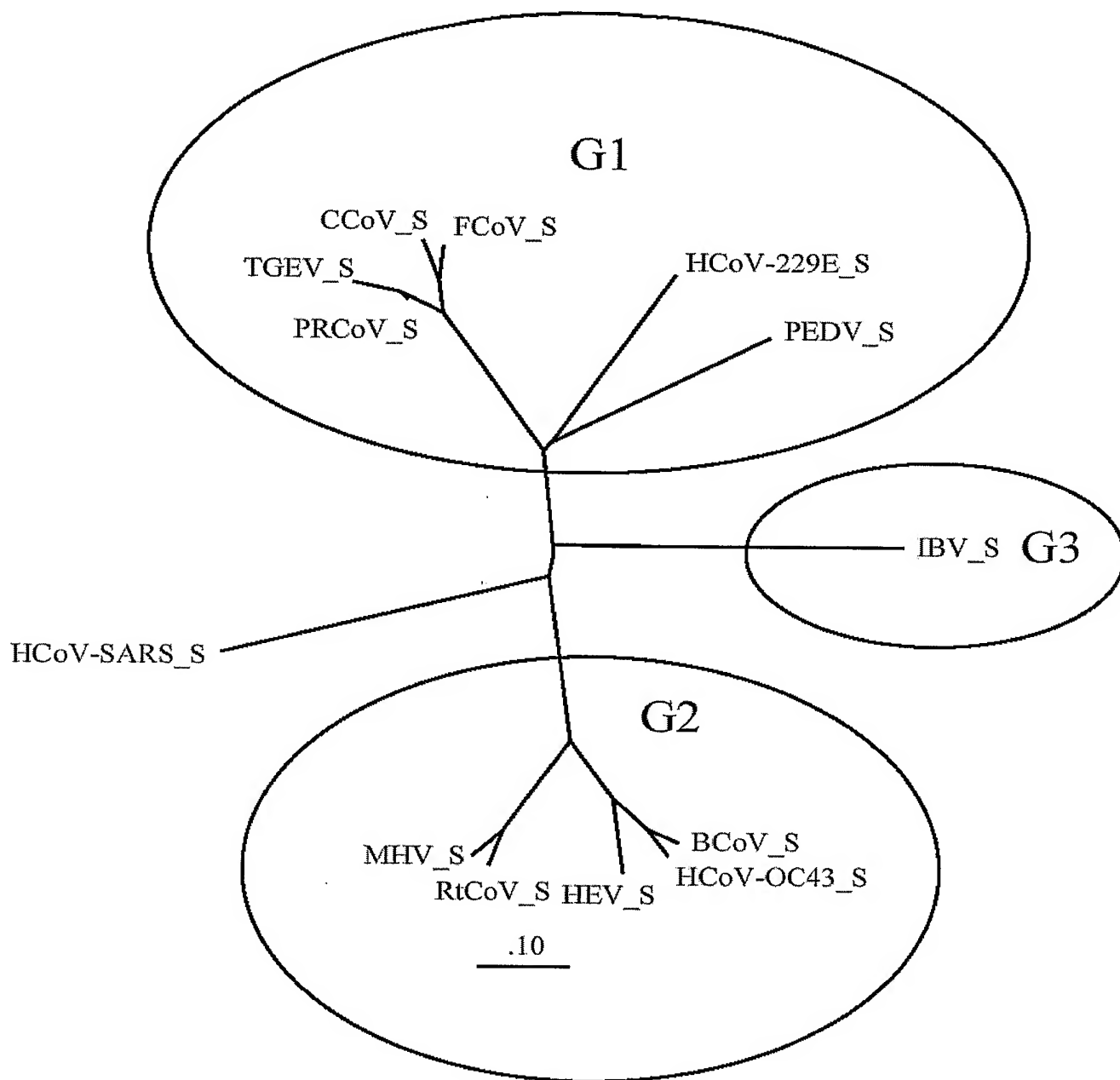
FIGURE 6**FIGURE 6A**

FIGURE 6B



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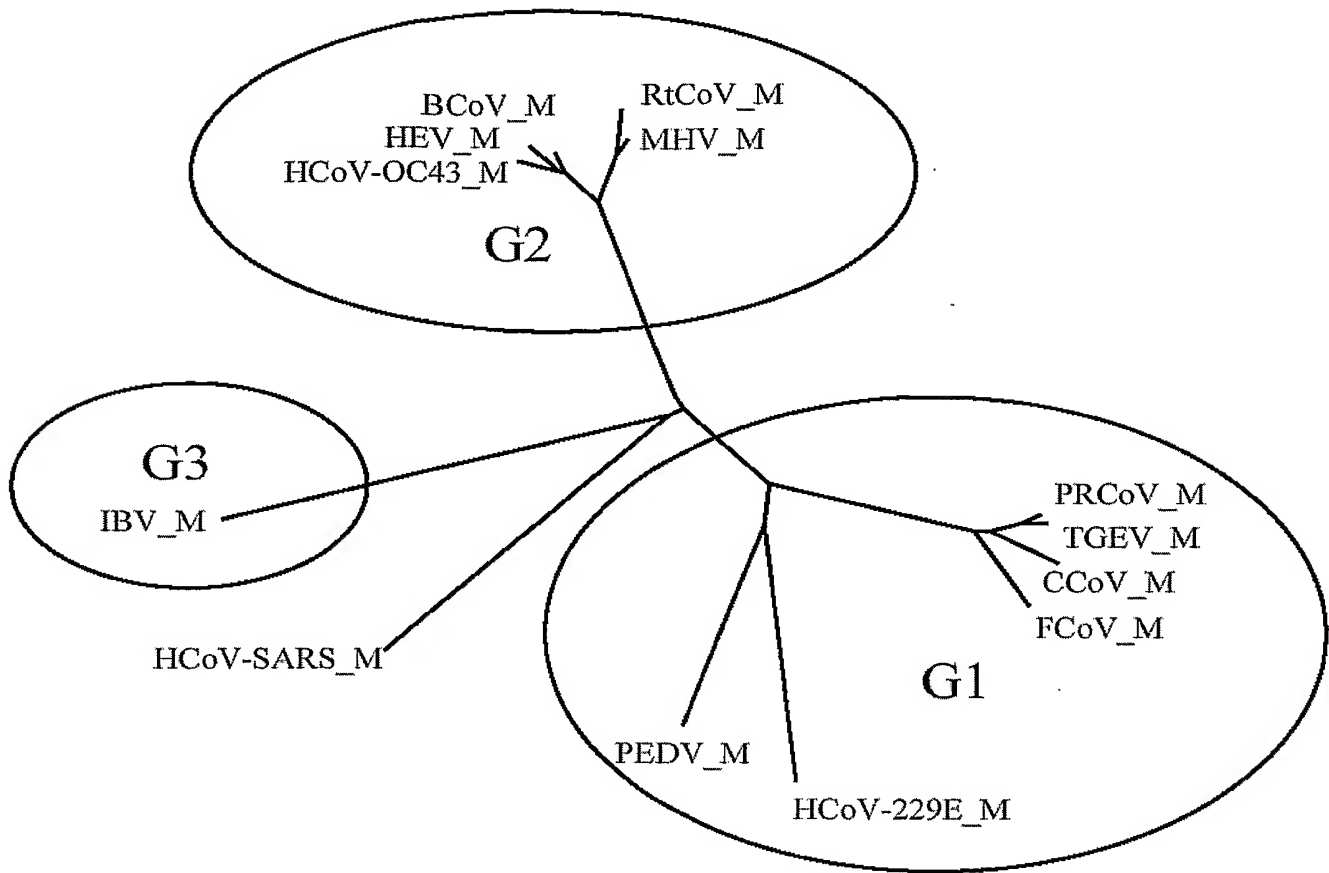
FIGURE 6C

FIGURE 7**FIGURE 7A**

```

SEQ ID NO:6053 -----MFVLLVAYALLH----- 12
SEQ ID NO:6057 ---MKKLFVVLVVMPLIYGDNFPCSKLTNRTIGNQWNLIETFLNYSRLPPNSDVVLGD 60
SEQ ID NO:6061 ---MRSLIYFWLLLPLVPTLSLPQDVTRCQSTTNFRFFSKFN-----VQAPAVVVLGG 52
SEQ ID NO:6065 -----MFLILLISLPTAFAVIGDLKCTTVS-INDVDTGVPSIS----- 38
SEQ ID NO:6069 -----MLFVFILFLPSCGLGYIGDFRCIQLVNSNGANVSAPSIS----- 40
SEQ ID NO:6042 -----MFIFLLFLTTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRG----- 39
SEQ ID NO:6072 -----MLVTPLLLVLTLLCALCSAVLYDSSS----- 27
      :. : .

SEQ ID NO:6053 ----- 120
SEQ ID NO:6057 YFPTVQPFNCIRNDSNDLYVTLENLKALYWDYATENITWNHRQRLNVVNGYPYSITVT 120
SEQ ID NO:6061 YLPSMNSSSWYCGTGIETASGVHGIFLSYIDSGQGFEIGISQEP-----FDPSGYQLYLH 107
SEQ ID NO:6065 -----TDTVDVTNGLGTYIYVLDREVLTLLNG-----YY 69
SEQ ID NO:6069 -----TETVEVSQGLGTYIYVLDREVLTLLNG-----YY 71
SEQ ID NO:6042 -----VYYPDEIFRSDTLTYLTQDLFLPFYSNVTGFHTINHTFG-----NP 79
SEQ ID NO:6072 -----YVYYYQSAFRPPSGWHLQG----- 46

SEQ ID NO:6053 -----IAGCQTTN-----GLNTSY SVCNG----- 31
SEQ ID NO:6057 TTRNFNSAEGAIICICKGSPPTTTTTESSLTCNWGSECLNHNKFPICPSNSEANCGNMLYG 180
SEQ ID NO:6061 KATNGNTNAIARLRICQFPDNTLGPVTNDVTGRNCLFNKAI PAYMRDGDIVVGITWD 167
SEQ ID NO:6065 PTSGSTYRNMALKGTLTLLSTLWFKPPFLSDFTNNGIFAKVKNKVIKDGVMYSEFPAITIG 129
SEQ ID NO:6069 PVDGSKFRNLALTGTNSVLSWFPQPPYLSQFNDGIFAKVQNLKSTPSGATAYFPTIVIG 131
SEQ ID NO:6042 VIPFKDGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINNSTNVVIRACNFELCDNPFFA 139
SEQ ID NO:6072 -----GAYAVVNISSEFNAGSSSGCTVGIHGGRVVNASSIAMTAP----- 88

SEQ ID NO:6053 ----- 240
SEQ ID NO:6057 LQWFADEVVAYLHGASYRISFENQWSGTVTFGDMRATTLEVAGTLVDLWWFNPVYDVSYY 240
SEQ ID NO:6061 -----NDRVTVFADKIIYHFLKNDWSRVATRCYNRRSCAMQVYVTPTYMLN----- 214
SEQ ID NO:6065 -----STFVNTSYSVVQPHTTILGNKLQGFLEISVCQYTMCEYPNT 171
SEQ ID NO:6069 -----SLFGYTSYTVVIEPN-----GVIMASVCQYTICLLPYT 165
SEQ ID NO:6042 VS-----KPMGTQHTMTMIFDNAFN----- 158
SEQ ID NO:6072 -----

SEQ ID NO:6053 -----CVGYSENVFAVESGGYIPSDFAFNNWFLLTNTSSVVDGVVRSF 74
SEQ ID NO:6057 RVNNKNGTTTVSNCTDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTK 300
SEQ ID NO:6061 VTSAGEDGIYYEPCTANCTGYAANVFATDSNGHIPEGFSFNNWFLLSNDSTLLHGKVSN 274
SEQ ID NO:6065 ICNPN-LGNQRVELWHWDTGVSCLYKRNFYDVNADYLYFHFYQEGGTFYAYFTDTGVV 230
SEQ ID NO:6069 DCKPNTNGNKLIGFWHTDVKPPICVLKRNFTLNVNADAFYFHFYQHGGTFYAYYADKPSA 225
SEQ ID NO:6042 -CTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFNTLK 217
SEQ ID NO:6072 -----SSGMAWSSSQFCTAHCNFSDTTVFVTHCYKHGG--CPLTGMLQON 131

SEQ ID NO:6053 QPLLLNCLWSVSGLRFTTGFFVYFNGTGRGDCCKGFSDDVLSDVIRYNLNFEEENLRRG---T 131
SEQ ID NO:6057 QPLLNVNCLWPVPSFEEAASTFCFEGAGFDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGAT 360
SEQ ID NO:6061 QPLLNVNCLLAIPKIYGLGQFFSFNHTMDGVCNGAAVDRAPEALRFNINDTSVILAEG--S 332
SEQ ID NO:6065 TKFLFNVLGTVLSHYVVMLTCN-----SALTLEYWVTPLTSTKQYLLAFNQDGVIFNAVD 286
SEQ ID NO:6069 TTFLFSVYIGDILTQYYVLPFICNPTAGSTFAPRYWVTPLVKRQYLFNFNQKVITSAMD 285
SEQ ID NO:6042 PIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITDAVD 277

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SEQ ID NO:6072 LIRVSAMKNGQLFYNLTVSVAKYPTFRSFQCVNNLTSVYLNGLVYTSNETIDVTSAGVY 191

SEQ ID NO:6053 ILFKTSYG----VVVFYCTNNT-LVSGDAHIPFGTVLGNFYCFVNTTIGNETTSFAVVGAL 186
 SEQ ID NO:6057 VFSLNTTGGVTLEISCYTVSDS-SFFSYGEIPFGVTDGPRYCYVHY---NGTALKYLGTL 416
 SEQ ID NO:6061 IVLHTALG---TNLSFVCSNSSDPLAIFAIPLGATEVPYYCFLKVDTYNSTVYKFLAVL 389
 SEQ ID NO:6065 CKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLNDKSVPS 345
 SEQ ID NO:6069 CASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVYRRVANLPACN-IEEWLTARSVPS 344
SEQ ID NO:6042 CSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVR-FPNITNLCPFGEVFNATKFPS 336
 SEQ ID NO:6072 FKAGGPITYKVMREVKALAYFVNGTAQDVILCDGSPRGLLACQYNTGNFSDGFYPFTNSS 251

SEQ ID NO:6053 PKTVREFVISRTGHFYINGYRYFTLGNEAVNFNVT----TAETTDFTCTVALASYADVLV 242
 SEQ ID NO:6057 PPSVKEIAISKWGHFYINGYNFFSTFPIDCISFNLT----TGDSDFVFTIAYTSYTEALV 472
 SEQ ID NO:6061 PPTVREIVITKYGDVYVNGFGYLHLGLLDAVTINFTGHGTTDDVSGFWTIAS TNFVDALI 449
 SEQ ID NO:6065 PLNWERKTFSNCFNMSSLSMFIQAYSFTCNNIDAA----KIYGMCFSSITIDKFAIPNG 401
 SEQ ID NO:6069 PLNWERKTQNCNFNLSLLRYVQAESLFCNNIDAS----KVYGRCFGSSISVDKFAVPRS 400
SEQ ID NO:6042 VYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSAT----KLNDLCFSNVYADSFVVKGD 392
 SEQ ID NO:6072 LVKQKFIVYRENSVNTTCTLHNFIFHNETGANPNPSG--VQNIQTYQTKTAQSGYYNFNF 309

SEQ ID NO:6053 NVSQTSIANIICYNSVINRLRCDQLSFDVPDGFYSTSP--IQSVELPVSIIVSLPVYHKHT 300
 SEQ ID NO:6057 QVENTAITKVTYCNSHVNNIKCSQITANLNGFYVPVSS--SEVGLVNKSVVLLPSFYTHT 530
 SEQ ID NO:6061 EVQGTISIQRILYCDDPVSQKCSQVAFDLDDGFYPISSRNLLSHEQPISEFVTLPSPNDHS 509
 SEQ ID NO:6065 RKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVS--VSRFNPSTWNRFRGFTEQS 459
 SEQ ID NO:6069 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVT--INNHNPPSSWNRRYGFNDAG 458
SEQ ID NO:6042 DVRQIAPGQTGVIADYNYKLPPDDFMGCVLAWNTRNIDAT-----STGNINYKYRYLRHG 446
 SEQ ID NO:6072 SFLSSSVYKESNFMYSYHPSCFRLETINGLWFNSLS-----VSIAYGPLQGGCKQS 363

SEQ ID NO:6053 FIVLYVDFKPQ-SGGGKCFNCYPAGVNITLANFNET---KGPLCVDTSHTFTKYVAVYAN 356
 SEQ ID NO:6057 IVNITIGLGMKRSGYGQPIASTLS--NITLPMQDHN---TDVYCIRSDQFS-VYVHSTCK 584
 SEQ ID NO:6061 FVNITVS-----AAFGLSSANLVASDTTNGFSS-----FCVDTRQFTITLFYNVTN 557
 SEQ ID NO:6065 VFKPQPAGVFTDHDVVYAQHCFASTNFCPCKLDGSLCVGNGPGIDAGYKTSIGITCPAG 519
 SEQ ID NO:6069 VFGKN-----QHDVVYAQQCFTRSSYCPC----- 483
SEQ ID NO:6042 KLRPFER----- 453
 SEQ ID NO:6072 VFKGRAT----- 370

SEQ ID NO:6053 VGRWS-----ASINTGNCPFSFGKVN NFVKFGSVCFS LKDIPGGCAMPIVA 402
 SEQ ID NO:6057 SALWDNIFKRNCTDVLDAVIKTGTCPPSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA 644
 SEQ ID NO:6061 SYGYVS-----KSQDSNCPFTLQSVNDYLSFSKFCVSTSLLAGACTIDLFG 603
 SEQ ID NO:6065 TNYLTCHNAAQCDCCLCTPDPTISKATGPYKCPQTKYLVGIGEHCSGLAIKSDHCG----G 575
 SEQ ID NO:6069 -----AQPDIVSPCTT---QTKPKSAFVNVDHCEGLGVLEDNCGNADPH 525
SEQ ID NO:6042 -----DISNVFFSPDGKPCPTPALNCYWPLND 480
 SEQ ID NO:6072 -----CCYAYSYGGPSLCKGVYSGELDHNFECEGL 399

SEQ ID NO:6053 NWAYSKY---YTIG-----SLYVSWSDGDGITGVPQVEGVSSFMNVTLDKC 446
 SEQ ID NO:6057 -RTRTNE---QVVR-----SLYVIYEEGDNIIVGVPSDNGSVHDL SVLHLDSC 687
 SEQ ID NO:6061 YPAFGSG---VKLT-----SLYFQFTKGELITGTPKPLEGITDV SFMTLDVC 647
 SEQ ID NO:6065 NPCTCQP---QAFLGWSVDSCLOGDRCNIFANFILHDVNSGTTCTSTD LQKSNTDIILGVC 632
 SEQ ID NO:6069 KGCICAN---NSFIGWSHDTC LVNDRQCIFANILLNGINS GTTCTSTD LQLPNT EVVTGIC 582
SEQ ID NO:6042 YGFYTTTGIGY-----QPYRVVLSFELLNAPATVCGPKLSTDLIKNQ 524
 SEQ ID NO:6072 LVYVTKS-----GGSRIQTATEPPVITQNNYNNITLNTC 433

| | | |
|-----------------------|--|-----------------|
| SEQ ID NO:6053 | ---RVAGRSAIEDILFSKLVTSGLGTVDADYKKCTKGLS--IADLACAQYYNGIMVLPGV | 739 |
| SEQ ID NO:6057 | ---KRKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGYD--IADLVCAQYYNGIMVLPGV | 1009 |
| SEQ ID NO:6061 | ---VVQKRSVIEDLLFNKVVTNGLGTVDEDYKRCSNGRS--VADLVCAQYYSGVMVLPGV | 942 |
| SEQ ID NO:6065 | ---KVSSRSAIEDLLFSKVKLSDBG-FVEAYNNCTGGAE--IRDLCVQSYNGIKVLPPPL | 963 |
| SEQ ID NO:6069 | GPSAIRGRSAIEDLLFDKVVKLSDBG-FVEAYNNCTGGQE--VRDLLCVQSFGNGIKVLPPV | 920 |
| SEQ ID NO:6042 | -----RSFIEDLLFNKVTLADAG-FMKQYGECLGDIN--ARDLICAKFNGLTIVLPPPL | 846 |
| SEQ ID NO:6072 | -----RSLIEDLLFTSVESVGLP-TNDAYKNCTAGPLGFFKDLCAREYNGLLVLPPI | 743 |
| | ** ***:** : . * * | ** *: **: *** : |

SEQ ID NO:6053 ADAERMAMYTGSLIGGIALGGLTS----AVSIPFSLAIQARLNLYVALQTDVLQENQKILA 795
SEQ ID NO:6057 ANADKMTMYTASLAGGITLGALGGG---AVAIPFAVAVQARLNLYVALQTDVLNKNQQILA 1066
SEQ ID NO:6061 VDAEKLHMYSASLIGGMALGGITA----AAALPFSYAVQARLNLYLALQTDVLQRNQQLLA 998
SEQ ID NO:6065 LSENQISGYTLAATSASLFPPWSA----AAGVPFYLNVQYRINGIGVTMDVLSQNQKILIA 1019
SEQ ID NO:6069 LSESQISGYTTGATAAAMFPPWSA----AAGVPFSLSVQYRINGLGVTMNVLSENQKMIA 976
SEQ ID NO:6042 LTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTONVLYENQKQIA 906
SEQ ID NO:6072 ITAEMQALYTSSLVASMAFGGITA----AGAIPFATQLQARINHLGITQSLLLKNQEKIA 799
* : . . . * : * : * : * : * : *

SEQ ID NO:6053 ASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQOGNSLNHLTSQLRQNF 855
SEQ ID NO:6057 SAFNQAIGNITQSFGKVNDAIHQTSRGLATVAKALAKVQDVVNIQGGALSHLTQVQLQNNF 1126
SEQ ID NO:6061 ESFNSAIGNITSFAVESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQLTVQLQHNF 1058
SEQ ID NO:6065 NAFNNALGAIQEGFDATN-----SALVKIQAVVNANAEALNNLLQQLSNRF 1065
SEQ ID NO:6069 SAFNNALGAIQDGFDAITN-----SALGKIQSVVNANAEALNNLLNQLSNRF 1022
SEQ ID NO:6042 NQFNKAISQIQESLTTTS-----TALGKLQDVVNQNAQALNTLVKQLSSNF 952
SEQ ID NO:6072 ASFNKAIGHMQEGFRSTS-----LALQQIQDVVSKQSAITLTETMASLNKNF 845
* : * : * : * : * : *

SEQ ID NO:6053 QAISSSIQAIYDRLDTIQADQQVDRLITGRLLAALNVFVSHLTITKYTEVRASRQLAQQKVN 915
SEQ ID NO:6057 QAISSSISDIYNRLDELSADAQVDRLITGRLLTALNAFVSQTLTRQAEVRASRQLAKDKVN 1186
SEQ ID NO:6061 QAISSSIDDIYSRLDILSADVQVDRLITGRLLSALNAFVAQTLTKYTEVQASRKLAQQKVN 1118
SEQ ID NO:6065 GAISSSLQEILSRLDALEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVN 1125
SEQ ID NO:6069 GAISASLQEILTRLEAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVN 1082
SEQ ID NO:6042 GAISSVLNDILSRLDKVEAEVQIDRLITGRLLQSLQTYVTQQLIRAAEIRASANLAATKMS 1012
SEQ ID NO:6072 GAISSVIQEIYQQFDAIQANAQVDRLITGRLLSVLASAKQAEYIRVSQORELATQKIN 905
* : * : * : * : * : *

SEQ ID NO:6053 ECVKSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCVDG---- 970
SEQ ID NO:6057 ECVRSQSQRFGFCG-NGTHLFLSLANAAPNGMIFHTVLLPTAYETVTAWPGICASDG-DR 1244
SEQ ID NO:6061 ECVKSQSQRFGFCGCGDGEHIFSLVQAAPQGLLFLHTVLPVPGDFVNVLAIAGLCVNG---- 1174
SEQ ID NO:6065 ECVKSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAG---- 1180
SEQ ID NO:6069 ECVKSQTTTRINFCG-NGNHILSLVQNAPYGLYFIHFSYVPISTTANVSPGLCISG---- 1137
SEQ ID NO:6042 ECVLGQSKRVDFCG-KGYHLMSPQAAPHGVFLHVTYVPSQERNFTTAPAICHEG---- 1067
SEQ ID NO:6072 ECVKSQSIRYSFCG-NGRHVLTIPQNAPEGIVFIHFSYTPDSFVNVTAVGFCVKPANAS 964
* : * : * : * : * : *

SEQ ID NO:6053 TNGYVLRQPNLALYK-----EGNYYRITSRIMFEPRIPTMAFVQIENCNVTFVNISRS 1024
SEQ ID NO:6057 TFGLVVKDVLTLFRN-----LDDKFYLTPTMYQPRVATSSDFVQIEGCDVLFVNATVS 1299
SEQ ID NO:6061 EIALTLREPGLVLFTHQLQTYTATEYFVSSRRMFEPKPTVSDVQIESCVVTVYNLTSD 1234
SEQ ID NO:6065 DRGIAPKSGYFVNINN-----TWMFTGSGYYPPEITGNNVVMSTCAVNYTKAPDV 1232
SEQ ID NO:6069 DRGLAPKAGYFVQDDG-----EWKFTGSSYYPPEITDKNSVIMSSCAVNYTKAPEV 1189
SEQ ID NO:6042 -KAYFPREGVVFVNGT-----SWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT 1118
SEQ ID NO:6072 QYAIVPANGRGIFIQVN-----GSYYITARDMYMPRAITAGDVVTLTSCQANYVSVNKT 1018
* : * : * : * : *

SEQ ID NO:6053 ELQTIPTV-EYIDVNKTLQELSYKL-PNYTVPDLVVEQYNQFILNLTSEISTLENKSAELN 1082
SEQ ID NO:6057 DLPSIIP-DYIDINQTVQDILENFRPNWTVPELTFDIFNATYLNLTGEIDDLFRSEKLN 1358
SEQ ID NO:6061 QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSPLPLDVFNATYLNLTGEIADLEQRSESLR 1292
SEQ ID NO:6065 MLNISTP-NLPYFKEELDQWFKNQTSVAPDLSLDY--INVTFDLQDEMNN----- 1279
SEQ ID NO:6069 FLNTSIP-NPPDFKEELDQWFKNQTSIAPDLSLDFEKLNVTLTLLDLYEMN----- 1238
SEQ ID NO:6042 VYDPLQP-ELDSFKEELDKYFKNHTSPDVLGDISG-INASVVNIQKEID----- 1166
SEQ ID NO:6072 VITTFVDNDDFDFNDELKSWWNTKHELPDFDKFN--YTVPIILDIDSEID----- 1066
* : * : * : * : *

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SEQ ID NO: 6053 YTVQKLQTLIDNINSTLVDLKWLN RVET YIKWPWWVWLCISVVLIFVVSMLLLCCSTGC 1142
 SEQ ID NO: 6057 NTTVELAILIDNINNTLVNLEWLNRIET YVKWPWYVWLLIGLVVIFCIPLLLFCCCSTGC 1418
 SEQ ID NO: 6061 NTTEELRSLINNINNTLV DLEWLN RVET YIKWPWWVWLIIVIVLIFVVSLLVFCCISTGC 1352
 SEQ ID NO: 6065 ----RLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWLLIGFAGVAMLVLLFFICCCTGC 1335
 SEQ ID NO: 6069 ----RIQDAIKKLNESYINLKEVGTYEMVVKWPWYVWLLIGLAGVAVCVLLFFICCCTGC 1294
SEQ ID NO: 6042 ----RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTILLCCMTSC 1222
 SEQ ID NO: 6072 ----RIQGVIOGLNDSLIDLEKLSILKTYIKWPWYVWLAIAFATIIIFILILGWVFFMTGC 1122
 .: . :*: .: :*: .: .: :*:***:*** : : : :*.*

SEQ ID NO: 6053 CGFFSCFA-----SSIRGCCESTKLPYYD-VEKIHQ--- 1173
 SEQ ID NO: 6057 CGCIGCLG-----SCCHSICSRQFENYEPIEKVHVH--- 1450
 SEQ ID NO: 6061 CGCCGCCG-----ACFSGCCRGPRLQPYEAFEKVHVQ--- 1384
 SEQ ID NO: 6065 G--TSCFK-----KCGGCCDDYTG HQELVIKT---SHED- 1364
 SEQ ID NO: 6069 G--SCCFK-----KCGNCCDEYGGHQDSIVIHNISSHED- 1326
SEQ ID NO: 6042 CSCLKGAC-----SCG-SCCKFDEDDSEPVLKGVLHYT- 1255
 SEQ ID NO: 6072 CGCCCGCFGIMPLMSKCGKSSYYTTFDNDVVT EQYRPKKS V 1164

FIGURE 7B

SEQ ID NO: 6054 -----MFLKLVDHHA-LVVNVLLWCVVLLIVILLVCITIIKLIKLCFTCHMFCNRTVY 51
 SEQ ID NO: 6062 -----MLQLVNDNG-LVVNVILWLVFLVFLLIISITFVQLVNLCTCHRLCNSAVY 54
 SEQ ID NO: 6058 ---MTFPRALTVIDDNG-MVINIIFWFLIIILILLSTALLNIIKLCMVCCNLGRTVII 59
SEQ ID NO: 6045 -----MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLV 52
 SEQ ID NO: 6073 -----MNLLNKSLEENG-SFLTALYIIIVGFLALYLLGRALQAFVQAADACCLFWYTWWV 57
 SEQ ID NO: 6066 -----MFADAYFADTVWVVGQIIFIVAICLLVLIIVVVAFLATFKLCIQLCGMCNTLVL 54
 : . : . . : : . . : :

SEQ ID NO: 6054 GP----IKNVYH-IY-QSYMH-----IDPF-----PKRVIDF----- 77
 SEQ ID NO: 6062 TP----IGRLYR-VY-KSYMR-----IDPL-----PSTVIDV----- 80
 SEQ ID NO: 6058 VP----AQHAYD-AY-KNFMR-----IKAYN-----PDGALLA----- 86
SEQ ID NO: 6045 KP----TVYVYS-RV-KNLNS-----SEGV-----PDLLV----- 76
 SEQ ID NO: 6073 IPGAKGTAFVYKYTYGRKLNNPELEAVIVNEFPKNGWNNKNPANFQDAQRDKLYS 112
 SEQ ID NO: 6066 SP----SIYVFN-RG-RQFYEF-----YNDVKP-----PVLDDVDV----- 84
 * : : . *

FIGURE 7C

SEQ ID NO: 6055 -----MSNDNC-----TGDIVTHLKNWNF 19
 SEQ ID NO: 6063 -----MSNGSIP-----VDEVIEHLRNWNF 24
 SEQ ID NO: 6059 ----MKILLILACVIACACGERYCAMSDFDLSCRNSTASDCESC FNGGDLIWHLANWNF 60
 SEQ ID NO: 6067 -----MSSVT-TPAPVYTWT-----ADEAIKFLKEWNF 27
 SEQ ID NO: 6070 -----MSSTQAPEPVYQWT-----ADEAVQFLKEWNF 33
SEQ ID NO: 6046 -----MADNGTIT-----VEELKQLLEQWNL 21
 SEQ ID NO: 6074 -----MPNETNCTLD-----FEQSVQLFKEYNL 28
 * . : :*:

SEQ ID NO: 6055 GWNVILTIFIVILQFGHYKYSRLFYGLKMLVLWLLWPLVLALSIFDTWANWDSN-WAFVA 78
 SEQ ID NO: 6063 TWNIILTILLVVLQYGHYKYSVFLYGVKMAILWILWPLVLALSIFDAWASFQVN-WVFFA 83
 SEQ ID NO: 6059 SWSIILIVFITVILQYGRPQFSWFVYGIKMLIMWLLWPVVLALTIFNAYSEYQVSRYVMFG 120
 SEQ ID NO: 6067 SLGIILLFITVILQFGYTSRSMFYVVKMILWLMWPLTIILTIFN--CVYALN-NVYL 84
 SEQ ID NO: 6070 SLGIILLFITIILQFGYTSRSMFYVVKMILWLMWPLTIVLCIFN--CVYALN-NVYL 90
SEQ ID NO: 6046 VIGFLFLAWIMLLQFAYSNRNRFLYIILVFLWLLWPLVLACFVLA--AVYRIN-WVTGG 78

SEQ ID NO:6074 FITAFLFLFTIILQYGYATRISKVIYTLKMIVLWCFWPLNIAVGVIS--CTYPPN-TGGLV 85
 :: : ** : . . . * : * : * : : : : . . .

SEQ ID NO:6055 FSFFMAVSTLVMWVMYFANSFRLFRRTFWAWNPEVNATVTTVL-GQTYQPIQQAPT 137
 SEQ ID NO:6063 FSILMACITLMLWIMYFVNSIRLWRRTHSWWSFNPETDALLTTSVM-GRQVCIPVLGAPT 142
 SEQ ID NO:6059 FSIAGAIVTFVLWIMYFVRSIQLYRRTKSWWSFNPETKAILCVSAL-GRSYVLPLEGVPT 179
 SEQ ID NO:6067 FSIVFTIVAIIMWIVYFVNSIRLFI RTGSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYH 143
 SEQ ID NO:6070 FSIVFTIVSIVIWIMYFVNSIRLFI RTGSWWSFNPETNNLMCIDMK-GTVYVRPIIEDYH 149
SEQ ID NO:6046 IAIA MACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLR-GTIVTRPLMESEL 137
 SEQ ID NO:6074 AAAILTVFACLSFVGYWIQSIRLFKRCRSWWSFNPESNAVGSILLTNGQQCNFAIESVPM 145
 :: : : : * : * : * : * : * : * : . : *

SEQ ID NO:6055 GITVTLLSGVLYVDGHRLASGVQVHNLPEYMTVAVPSTTIISRVGRSVNSQNSTG--WV 195
 SEQ ID NO:6063 GVTLTLLSGTLLVEGYKVATGVQVSQLPNFVTVAKATTTIVYGRVGRSVNASSGTG--WA 200
 SEQ ID NO:6059 GVTLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLVGKKLKASSATG--WA 237
 SEQ ID NO:6067 TLTVTIIRGHLYMQGIKLTGYSLSDLPAYVTVAKVSHLLTYKRG-FLDKIGDTS--FA 200
 SEQ ID NO:6070 TLTATIIRGHLYMQGVKLTGTFSLSDLPAYVTVAKVSHLCTYKRA-FLDKVDGVSG--FA 206
SEQ ID NO:6046 VIGAVIIRGHLMAGHSLGR-CDIKDLPKEITVATS-RTLSYYKLGASQVRVGTDSG--FA 193
 SEQ ID NO:6074 VLSPIIKNGVLYCEGQWLAK-CEPDHLPKDFVCTPDRRNIYRMVQKYTGDSGNKKRFA 204
 : : * * * : . . . ** : * . * . . . :

SEQ ID NO:6055 FYVRVKHGDFS AVSSPMSNMTENERLLHFF 225
 SEQ ID NO:6063 FYVRSKHGDYSAVSNSAVLTDSEKVLHLV 230
 SEQ ID NO:6059 YYVKS KAGDYSTEAR-TDNLSEQEKLLHMV 266
 SEQ ID NO:6067 VYVKS KVGNYRLPSTQKGSGLDTALLRNNI 230
 SEQ ID NO:6070 VYVKS KVGNYRLPSN-KPSGADTALLR--I 233
SEQ ID NO:6046 AYNRYRIGNYKLNTHAGSNDNIALIVQ-- 221
 SEQ ID NO:6074 TFVYAKQSVDTGELESVATGSSSLYT---- 230
 : : . . .

FIGURE 7D

SEQ ID NO:6056 -----MATVKWADASE-----PQRGRQG----- 18
 SEQ ID NO:6064 -----MASVSF-----QDRGRK----- 17
 SEQ ID NO:6060 -----MANQGQRVSWGDEST-----KTRGRSNSRGRKN----- 31
 SEQ ID NO:6068 MSFTPGKQSSS-RASSGNRSGNGILK---WADQSDQSRNVQTRGRR-AQPKQTATSQQPS 55
 SEQ ID NO:6071 MSFVPGQENAGGRSSSVNRAGNGILKKTWADQTERGPNNQNRGRR-NQPKQTATTQ-PN 58
SEQ ID NO:6051 -----MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN 48
 SEQ ID NO:6075 -----MASGKAAGKTDA PAPVIKLGPKP-----PKVGSS----- 35
 . . . *

SEQ ID NO:6056 ----RIPYSLYSPLLVDSEQPW-KVIPRNLVPINKK-DKNKLIGYWN--VQKRFRTRK GK 70
 SEQ ID NO:6064 ----RVPLSLYAPLRVTNDKPLSKVLANNAVPTNKG-NKDQQIGYWN--EQIRWRMRGE 70
 SEQ ID NO:6060 ---NNIPLSFFNPITLQQGSKFWNLCP RDFVPKGIG-NRDQQIGYWN--RQTRYRMVKGQ 85
 SEQ ID NO:6068 GGNVVPYYSWFSGITQFQKGKEFEFAEQGVPIAPGVPATEAKGYWYRHNRRSFKTADGN 115
 SEQ ID NO:6071 SGSVVPYYSWFSGITQFQKGKEFQFAEQGVPIANGIPASEQKGYWYRHNRRSFKTPDGQ 118
SEQ ID NO:6051 NT-----ASWFTALTQH GK-EELRFRQGQVPINTNSGPDDQIGYRRATRR-VRGGDGK 101
 SEQ ID NO:6075 -----GNASWFQAIKAKKLNTPPPKFEGSGVPD NENIKPSQQHGYWR--RQARFKPGKGG 88
 * : : . ** . ** : : *

SEQ ID NO:6056 RVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKTEPTGYGVR RNKSEPEIPHFN 130
 SEQ ID NO:6064 RIEQPSNWHFYLLGTGPHGDLRYRTRTEGVFWVAKEGAKTEPTNLGVRKASEKPIIPKFS 130
 SEQ ID NO:6060 RKELPERWFFYYLGTGPHADAKFKDKLDGVVWVAKD GAMNKPTTLGSRGANNESKALKFD 145
 SEQ ID NO:6068 QRQLLPRWYFYLLGTGPHAKDQYGTDDIDGVYVWASNQADVNT PADILDRDPSSD--EAIP 173

SEQ ID NO:6071 QKQLLPRWYFYLLGTGPHAGASYGDSIEGVFWVANSQADTNTRSDIVERDPSSH--EAIP 176
SEQ ID NO:6051 MKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN--AATV 159
SEQ ID NO:6075 RKPVPDAWYFYTTGTGPAADLNWGDQTQDGIVWVAAGADTKSRSNQGTDRDPDKF--DQYP 146
 *** **** : *: *** . * ..

SEQ ID NO:6056 QKLPNGVTVVEE---PDSRAPSRSSQSR-----SQSRGRGESK----- 164
SEQ ID NO:6064 QQLPSVVEIVEPNTTPPASRANSRSTRSGNGNRSRSPSNNRGNNQSRGNSQNRGNNQGRG 190
SEQ ID NO:6060 GKVPGEFQLEVN---QSRDNSRSRSQ-----SRSRSRNR----- 176
SEQ ID NO:6068 TRFPFGTVLPQGYIEGS-GRSAPNSR-----STSRASSRASS----- 210
SEQ ID NO:6071 TRFAPGTVLPQGFYVEGS-GRSAPASR-----SGSRSSQSRGP----- 212
SEQ ID NO:6051 LQLPQGTTLPKGFYAEGRSGGSQASSR-----SSSRSGNSR----- 196
SEQ ID NO:6075 LRFSDGGPDGNFRWDFIPLNRGRSGRS-----TAASSAAASR----- 183
 :.. . . : . .

SEQ ID NO:6056 -----PQSRNPSSDRNHN-----SQDDIMKAVAAALKSLGFDKPKQEKDKKS 205
SEQ ID NO:6064 ASQNRGGMNMMNKSQRNQSNNRNQSNDRGGVTSRDDLVAAVKDALKSLGIGENPDRHKQ- 249
SEQ ID NO:6060 -----SQSRGRQGFNNKK-----DDSVEQAVLAALKKLGVDTKEQQORS- 215
SEQ ID NO:6068 -----AGSRSRANSNRT-----PTSGVTPDMADQIASLVLA KL GKDAAKP 251
SEQ ID NO:6071 -----NNRARSSSNQRQ-----PASTVKPDMAEETAAVLAKL GK DAGQP 252
SEQ ID NO:6051 -----NSTPGSSRGNS-----PARMASGGGETALALLLLDRLNQLSKV 235
SEQ ID NO:6075 -----APSREGSRGRR-----SDSGDDLIARA AK I IQDQ----- 212
 : .

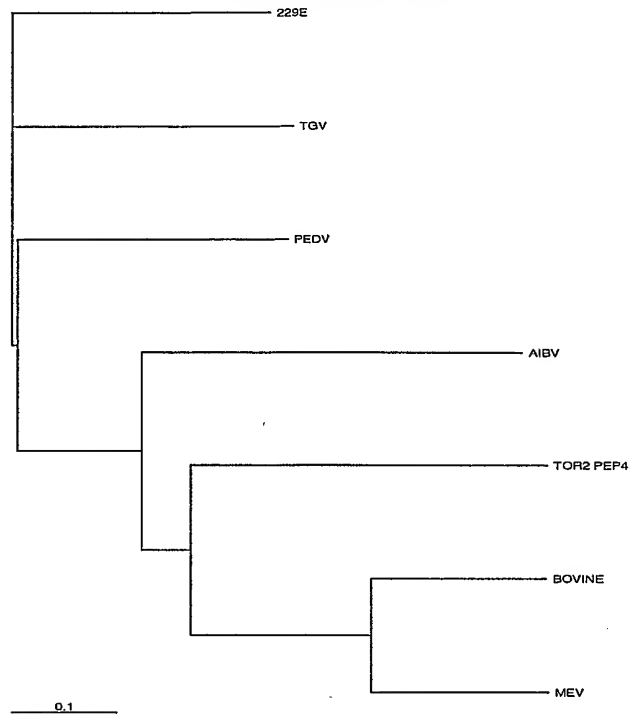
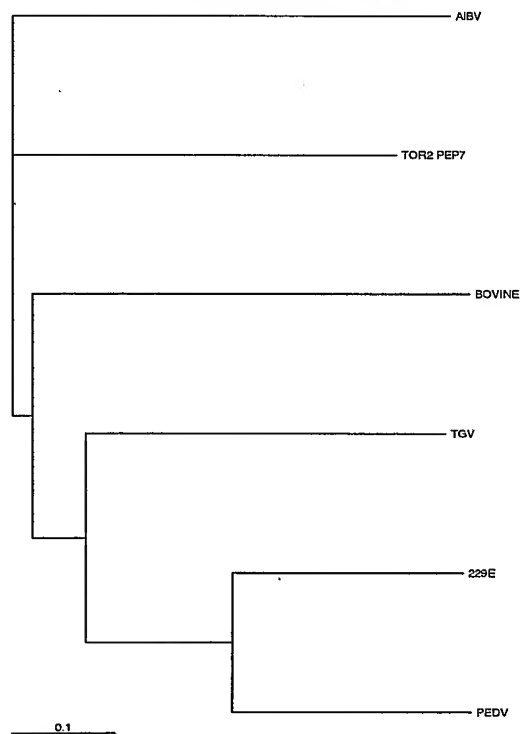
SEQ ID NO:6056 AKTGTPKPSRNQSPASSQTS AKSLARSQSSETKEQKHEMQKPRWKRPND DVTSNVTQCF 265
SEQ ID NO:6064 ----QKPKQEKSDNSGKNTPK---KNKS RATS KERDLKD IPEWRRIPKG--ENSVAACF 300
SEQ ID NO:6060 ----RSKSKERSNSKTRDTPK-----NENKHTWKRTAGK---GDVTRFY 253
SEQ ID NO:6068 ----QOVTKQTAKEIRQKILN-----KPRQKRSPNK---QCTVQOCF 286
SEQ ID NO:6071 ----KQVTKQSAKEVRQKILN-----KPRQKRTPNK---QCPVQOCF 287
SEQ ID NO:6051 SGKGQQQQGQTVTKKSAEASK-----KPRQKRTATK---QYNVTQAF 275
SEQ ID NO:6075 ----QKKS RITKAKADEMAH-----RRYCKRTIPP---NYRVDQVF 247
 : : : *

SEQ ID NO:6056 GPRDLDH---NFGSAGVVANGVKAGYPQFAELVPSTAAMLFD SHIVSKESG----- 314
SEQ ID NO:6064 GPRGGFK---NFGDAEFVEKGVDASGYAQIASLAPNVAALLFGGNVAVRELA----- 349
SEQ ID NO:6060 GARSSSA---NFGD TDLVANGSSAKHYPQLAECVPSVSSILFGSYWTSKEDG----- 302
SEQ ID NO:6068 GKRGPNQ---NFGGGEMLKLGTSDPQFPILAE LAPTAGAFFFGSRLELAKVQNL SGNLDE 343
SEQ ID NO:6071 GKRGPNQ---NFGGSEMLKLGTSDPQFPILAE LAPT VG AFFFGSKLELVKKN---SGGADE 342
SEQ ID NO:6051 GRRGPEQTQGNFGDQDLIRQGT DYKHWPQIAQFAPSASAFFGMSRIGMEVTP----- 327
SEQ ID NO:6075 GPRTKGK-EGNFGDDKMNEEGIKDGRVTAMLNLVPSSHACLF GSRVTPKLQL----- 298
* * *** . * . : . *. : .

SEQ ID NO:6056 ---NTVVLTFTTRVTVPKDHP---HLGKFLEELNAFTR-----EMQ 349
SEQ ID NO:6064 ---DSYEITYNYKMTVPKSDP---NVELLVSQVDAFKTGN AK-LQRKKEKKNKRETTLO 401
SEQ ID NO:6060 ---DQIEVTFTHKYHLPKDDP---KTGQFLQQINAYAR-----PSEVAKEQR 343
SEQ ID NO:6068 PQKD VYELRYNGAIRFDSTLSGFETIMKVLNENLNAYQQQD---GTMMNSPKPQRQ--R 397
SEQ ID NO:6071 PTKDVYELQYSGAVRFDSTLPGFETIMKVLNENLNAYQKDG---GADVSPKPKQRKGRR 398
SEQ ID NO:6051 ---SGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFP---PTE----- 368
SEQ ID NO:6075 ---DGLHLRFETTVVPCDDPQFDNYVKICDQCVDGVGTRPKDDEPKPKSRSSSRPATRG 355
 . : : . . : .

SEQ ID NO:6056 QHPLLNP SALEFNPSQTSP-----ATAEPVRDEVSIETDIIDEVN----- 389
SEQ ID NO:6064 QHEEA IYDDVGAPSDVTHANLEWDTAVDGGDTAVEIINEIFDTGN----- 446
SEQ ID NO:6060 KRKSRSKSAERSEQDVVPDALIENYTDVDDTQVEIIDEVTN----- 385
SEQ ID NO:6068 GQKNGQGENDNISVAAPKSRVQONKIRELTAEDISLLKKMDEP-----FTEDTSEI--- 448
SEQ ID NO:6071 QAQEKKDEVDNVSVAKPKSSVQRNVSRELTPEDRSLLAQILDDGVVPDGLEDDSNV--- 454

SEQ ID NO:6051 -PKKDKKKKTDEAQPLPQRQKKQPTVTLLPAA----- 399
SEQ ID NO:6075 NSPAPRQQRPKKEKKLKKQDDEADKALTSDEERNNAQLEFYDEPKVINWGDAALGENEL 414

FIGURE 7E**FIGURE 7F**

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FIGURE 7G

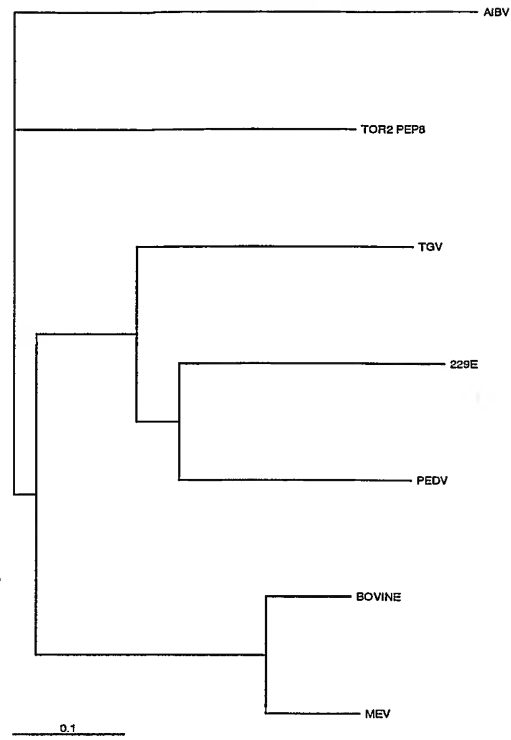


FIGURE 7H

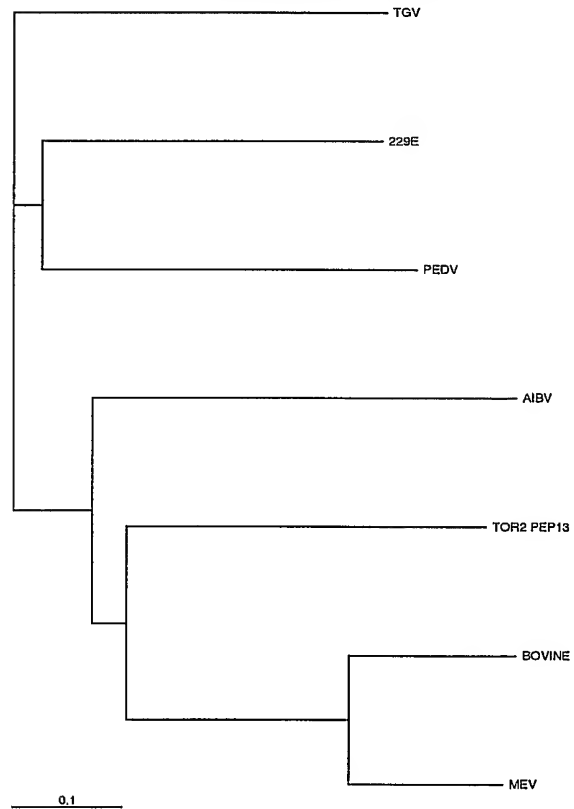


FIGURE 8

| | | | | | | |
|------------------------------|-------|---|-----|-----|-----|-----------|
| | | | | | | Section 1 |
| | (1) | 1 | 10 | 20 | 30 | 42 |
| avian IBV partial 5'UTR 161- | (1) | TATTAATAATCTTATTGTTGCTGGTATCACTGCTTGTGTTTGGCC | | | | |
| HCoV-OC43 5'UTR | (1) | ----- | | | | |
| bovine CV 5'UTR | (1) | ----- | | | | |
| Consensus | (1) | | | | | |
| | | | | | | Section 2 |
| | (43) | 43 | 50 | 60 | 70 | 84 |
| avian IBV partial 5'UTR 161- | (43) | GTGTCTCACTTTATACATCTGTTGCTTGGGCTACCTAGTGTC | | | | |
| HCoV-OC43 5'UTR | (1) | ----- | | | | |
| bovine CV 5'UTR | (1) | ----- | | | | |
| Consensus | (43) | | | | | |
| | | | | | | Section 3 |
| | (85) | 85 | 90 | 100 | 110 | 126 |
| avian IBV partial 5'UTR 161- | (85) | CAGCGTCCTACGGGCGTCGTGGCTGGTTCGAGTGCGAGGAAC | | | | |
| HCoV-OC43 5'UTR | (1) | ----- | | | | |
| bovine CV 5'UTR | (1) | ----- | | | | |
| Consensus | (85) | | | | | |
| | | | | | | Section 4 |
| | (127) | 127 | 140 | 150 | | 168 |
| avian IBV partial 5'UTR 161- | (127) | CTCTGGTTTCATCTAGCGGTAGGCGGGTGTGTGGAAGTAGCAC | | | | |
| HCoV-OC43 5'UTR | (1) | -----GATTGTGAGCGATTTCGCTGCGTGCA--TCCCGC | | | | |
| bovine CV 5'UTR | (1) | -----GATTGCGAGGGATTTCGGTGCGTGCA--TCCCGC | | | | |
| Consensus | (127) | GATTG GAGCGATTTCGCTGCGTGCA TCCCGC | | | | |
| | | | | | | Section 5 |
| | (169) | 169 | 180 | 190 | 200 | 210 |
| avian IBV partial 5'UTR 161- | (169) | TTCA GACGTACCGGTTCTGTGTGAAATA--CGGGGTAC | | | | |
| HCoV-OC43 5'UTR | (33) | TTCA-----CTGATCTCTTGTTAGATCTTTTGTAAATCTA | | | | |
| bovine CV 5'UTR | (33) | TTCA-----CTGATCTCTTGTTAGATCTTTTCATAATCTA | | | | |
| Consensus | (169) | TTCA CTGATCTCTTGTTAGATCTTTTCGTAATCTA | | | | |
| | | | | | | Section 6 |
| | (211) | 211 | 220 | 230 | 240 | 252 |
| avian IBV partial 5'UTR 161- | (209) | CTCCCCCACATACCTCTAAGGGCTTTTGAGCCTAGCGTTGG | | | | |
| HCoV-OC43 5'UTR | (68) | AACTTTTATAAAAAACATCCACTCCCTGTAATCTATGCTTGTGG | | | | |
| bovine CV 5'UTR | (68) | AACTTTTATAAAAAACATCCACTCCCTGTAAGTCTATGCCTGTGG | | | | |
| Consensus | (211) | AACTTTTATAAAAAACATCCACTCCCTGTAAGTCTATGCCTGTGG | | | | |
| | | | | | | Section 7 |
| | (253) | 253 | 260 | 270 | 280 | 294 |
| avian IBV partial 5'UTR 161- | (251) | GCTACGTTCTCGCATAAGGTCGGCTATACGAGGTTTGTAGGG | | | | |
| HCoV-OC43 5'UTR | (110) | GCGTAGATTTTTCATAGTGGTGTCTATATT-CATTTCT-GCT | | | | |
| bovine CV 5'UTR | (110) | GCGTAGATTTTTCATAGTGGTGTCTATATT-CATTTCT-GCT | | | | |
| Consensus | (253) | GCGTAGATTTTTCATAGTGGTGTCTATATT CATTTCT GCT | | | | |
| | | | | | | Section 8 |
| | (295) | 295 | 300 | 310 | 320 | 336 |
| avian IBV partial 5'UTR 161- | (293) | GGTAGTGCCAAACAACCCCTGAGGTGACAGGTTCTGGTGGTG | | | | |
| HCoV-OC43 5'UTR | (150) | GTTAACAGCTTTTCAGCCAGGGACGTGTTGTATCCTAGGC--- | | | | |
| bovine CV 5'UTR | (150) | GTTAACAGCTTTTCAGCCAGGGACGTGTTGTATCCTAGGC--- | | | | |
| Consensus | (295) | GTTAACAGCTTTTCAGCCAGGGACGTGTTGTATCCTAGGC | | | | |
| | | | | | | Section 9 |
| | (337) | 337 | 350 | 360 | | 373 |
| SEQ ID NO: 9910 | (335) | TTTAGTGAGCAGACATACAATAGACAGTGACAACATG | | | | |
| SEQ ID NO: 9919 | (189) | ---AGTG-GCCCGCCCATAGGTCACAATG----- | | | | |
| SEQ ID NO: 9892 | (189) | ---AGTG-GCCCACCCATAGGTCACAATG----- | | | | |
| Consensus | (337) | AGTG GCCCACCCATAGGTCACAATG | | | | |

FIGURE 9

| SEQ ID NO: | | |
|--|--------------|-------------|
| F1: AT $\frac{\text{CTT}}{\text{TGC}}$ G $\frac{\text{C}}{\text{A}}$ G $\frac{\text{GT}}{\text{CG}}$ A $\frac{\text{GGC}}{\text{TTT}}$ G $\frac{\text{G}}{\text{C}}$ GTG | (136-154 nt) | 6021 |
| F2: GTG $\frac{\text{T}}{\text{C}}$ GTG $\frac{\text{G}}{\text{C}}$ AT $\frac{\text{AG}}{\text{CC}}$ C $\frac{\text{A}}{\text{G}}$ CTTCA | (152-172 nt) | 6022 |
| F3: CTTCAC $\frac{\text{G}}{\text{T}}$ G $\frac{\text{T}}{\text{A}}$ TCT $\frac{\text{G}}{\text{C}}$ TTGT $\frac{\text{GT}}{\text{TA}}$ GA | (168-195nt) | 6023 |
| R1: AG $\frac{\text{A}}{\text{G}}$ A $\frac{\text{CCTGT}}{\text{TACAA}}$ CAC $\frac{\text{C}}{\text{G}}$ TC $\frac{\text{AGG}}{\text{CCT}}$ GG $\frac{\text{T}}{\text{C}}$ TG | (307-329nt) | 6024 |
| R2: AAA $\frac{\text{C}}{\text{T}}$ G $\frac{\text{CG}}{\text{AA}}$ TATA $\frac{\text{GC}}{\text{AA}}$ C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG | (265-288nt) | 6025 |
| R3: C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG $\frac{\text{CG}}{\text{AA}}$ A $\frac{\text{G}}{\text{A}}$ A $\frac{\text{A}}{\text{T}}$ C $\frac{\text{GTA}}{\text{TAC}}$ GCCCA | (250-274nt) | 6026 |

FIGURE 10

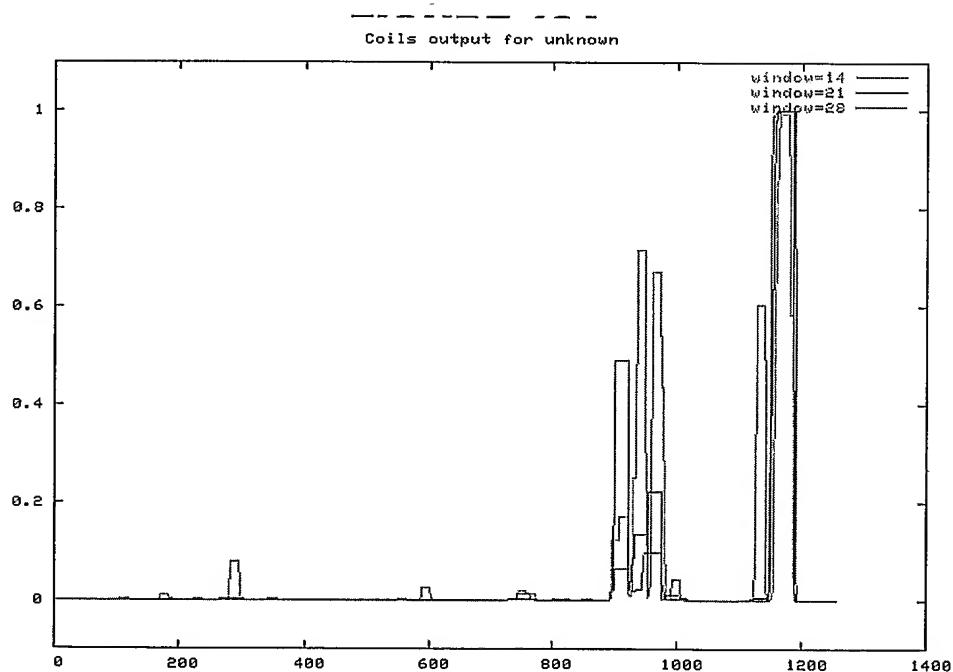
| | | | | | |
|------------------------------------|-------|---------------------------------------|-----|-----|---------|
| | | Section 1 | | | |
| | (1) | 1 | 10 | 20 | 36 |
| avian IBV 3'UTR (NC_001451) 27103- | (1) | GTAACATAATGGACCTGTTGTTTCCTGGTACATTTT | | | |
| HCoV-OC43 3'UTR partial | (1) | ----- | | | |
| bovine CV 3'UTR | (1) | ----- | | | |
| Consensus | (1) | | | | |
| | | Section 2 | | | |
| | (37) | 37 | 50 | 60 | 72 |
| avian IBV 3'UTR (NC_001451) 27103- | (37) | GTTAAACACTATTTCTGTGCTTTCCTATCAATTATT | | | |
| HCoV-OC43 3'UTR partial | (1) | ----- | | | |
| bovine CV 3'UTR | (1) | ----- | | | |
| Consensus | (37) | | | | |
| | | Section 3 | | | |
| | (73) | 73 | 80 | 90 | 108 |
| avian IBV 3'UTR (NC_001451) 27103- | (73) | ACAGGCATTGATTGTGATTATGTTCAATACTTAAGC | | | |
| HCoV-OC43 3'UTR partial | (1) | ----- | | | |
| bovine CV 3'UTR | (1) | ----- | | | |
| Consensus | (73) | | | | |
| | | Section 4 | | | |
| | (109) | 109 | 120 | 130 | 144 |
| avian IBV 3'UTR (NC_001451) 27103- | (109) | TTCTTTTGGTTGCTTTTGGCTTATTGTATTGTTGCT | | | |
| HCoV-OC43 3'UTR partial | (1) | ----- | | | |
| bovine CV 3'UTR | (1) | ----- | | | |
| Consensus | (109) | | | | |
| | | Section 5 | | | |
| | (145) | 145 | 150 | 160 | 170 180 |
| avian IBV 3'UTR (NC_001451) 27103- | (145) | GTGCTTTTTTATTGTTGTGATTCTCATTAGTTTG--C | | | |
| HCoV-OC43 3'UTR partial | (1) | -----TAAGAGAATGAAC | | | |
| bovine CV 3'UTR | (1) | -----GAGAATGAAC | | | |
| Consensus | (145) | A GAGAATGAAC | | | |
| | | Section 6 | | | |
| | (181) | 181 | 190 | 200 | 216 |
| avian IBV 3'UTR (NC_001451) 27103- | (179) | TTTATCGTAGAAATTCAATAGTAAGAGTTAAGGGAAG | | | |
| HCoV-OC43 3'UTR partial | (14) | CTTAT-GTCGGCACCTGGTGSTAAACCCCTC-GCAGG | | | |
| bovine CV 3'UTR | (11) | CTTAT-GTCGGCACCTGGTGSTAAACCCCTC-GCAGG | | | |
| Consensus | (181) | CTTAT GTCGGCACCTGGTGSTAAACCCCTC GCAGG | | | |
| | | Section 7 | | | |
| | (217) | 217 | 230 | 240 | 252 |
| avian IBV 3'UTR (NC_001451) 27103- | (215) | ATAGGCATGTAGCTTGATTACCTACATGTCTATCGC | | | |
| HCoV-OC43 3'UTR partial | (48) | AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG | | | |
| bovine CV 3'UTR | (45) | AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG | | | |
| Consensus | (217) | AAAGTCGGG ATAAGGCAC TCTCTATCAG | | | |

FIGURE 10 (contd.)

| | | | | | | |
|------------------------------------|-------|--------------------------------------|-------------------------|-----------------|-------------|-----|
| | | | | | Section 8 | |
| | (253) | 253 | 260 | 270 | 288 | |
| avian IBV 3'UTR (NC_001451) 27103- | (251) | CAGGGAAATGTC | TAATCTGTC | TACTTAGTAGCCTGG | | |
| HCoV-OC43 3'UTR partial | (76) | AATGGA | --TGTCTTGCTGCTATAA | TAGATAGA--- | G | |
| bovine CV 3'UTR | (73) | AATGGA | --TGTCTTGCTGCTATAA | TAGATAGA--- | G | |
| Consensus (253) | | AATGGA | TGTCTTGCTGCTATAA | TAGATAGA | G | |
| | | | | | Section 9 | |
| | (289) | 289 | 300 | 310 | 324 | |
| avian IBV 3'UTR (NC_001451) 27103- | (287) | AAACGAACGG | CTAGACCCCTAGATT | TTAATTTAGTTT | | |
| HCoV-OC43 3'UTR partial | (107) | AAGGTTATAGCAGACTAT | -AGATT--- | AATTAGTTG | | |
| bovine CV 3'UTR | (104) | AAGGTTATAGCAGACTAT | -AGATT--- | AATTAGTTG | | |
| Consensus (289) | | AAGGTTATAGCAGACTAT | AGATT | AATTAGTTG | | |
| | | | | | Section 10 | |
| | (325) | 325 | 330 | 340 | 350 | 360 |
| avian IBV 3'UTR (NC_001451) 27103- | (323) | AAATTTT | TTAGTTT | AGTTTAAAGTTAGT | -TTAGAGTAGG | |
| HCoV-OC43 3'UTR partial | (139) | AAAGTTT | TGTGTGTAATGTATAGT | GTTGGAGAAAG | | |
| bovine CV 3'UTR | (136) | AAAGTTT | TGTGTGTAATGTATAGT | GTTGGAGAAAG | | |
| Consensus (325) | | AAAGTTT | TGTGTGTAATGTATAGT | GTTGGAGAAAG | | |
| | | | | | Section 11 | |
| | (361) | 361 | 370 | 380 | 396 | |
| avian IBV 3'UTR (NC_001451) 27103- | (358) | TATAAAGATGCCAGT | TGCCGGGGCCAC | -GCCGAGTAC | | |
| HCoV-OC43 3'UTR partial | (175) | TG-AAAGACT--- | TGCCGGAAGTAATTGCCGACAAG | | | |
| bovine CV 3'UTR | (172) | TG-AAAGACT--- | TGCCGGAAGTAATTGCCGACAAG | | | |
| Consensus (361) | | TG AAAGACT | TGCCGGAAGTAATTGCCGACAAG | | | |
| | | | | | Section 12 | |
| | (397) | 397 | 410 | 420 | 432 | |
| avian IBV 3'UTR (NC_001451) 27103- | (393) | GATCGAGGGTACAGCACTAGGACG | CCCCATTAGGGGA | | | |
| HCoV-OC43 3'UTR partial | (206) | TGCCCAAAGGGGAAGAGCCAGCAG | ---- | TTAAGTTA | | |
| bovine CV 3'UTR | (203) | TGCCCAAAGGGGAAGAGCCAGCATG | ---- | TTAAGTTA | | |
| Consensus (397) | | TGCCCAAAGGGGAAGAGCCAGCAG | | TTAAGTTA | | |
| | | | | | Section 13 | |
| | (433) | 433 | 440 | 450 | 468 | |
| avian IBV 3'UTR (NC_001451) 27103- | (429) | AGAGCTAAATTTTAGT | --TTAAGTTAAGTTTAAAT | -T | | |
| HCoV-OC43 3'UTR partial | (238) | CCACCCAGTAATTAGTAAATGAATGAAGTTAATTAT | | | | |
| bovine CV 3'UTR | (235) | CCATCCAGTAATTAGTAAATGAATGAAGTTAATTAT | | | | |
| Consensus (433) | | CCA CCAGTAATTAGTAAATGAATGAAGTTAATTAT | | | | |
| | | | | | Section 14 | |
| | (469) | 469 | 480 | 490 | 504 | |
| avian IBV 3'UTR (NC_001451) 27103- | (462) | GGCTAAGTATAGTTAAAATTTATAGGCTAGTATAGA | | | | |
| HCoV-OC43 3'UTR partial | (274) | GGCCAATTGGAAGAATCAC | ----- | | | |
| bovine CV 3'UTR | (271) | GGCCAATTGGAAGAATCAC | ----- | | | |
| Consensus (469) | | GGCTAAGTATAGTTAAAATTTATAGGCTAGTATAGA | | | | |
| | | | | | Section 15 | |
| | (505) | 505 | 513 | | | |
| avian IBV 3'UTR (NC_001451) 27103- | (498) | GTTAGAGCA | | SEQ ID NO: 9911 | | |
| HCoV-OC43 3'UTR partial | (293) | ----- | | SEQ ID NO: 9920 | | |
| bovine CV 3'UTR | (290) | ----- | | SEQ ID NO: 9893 | | |
| Consensus (505) | | | | | | |

FIGURE 11**SEQ ID NO:**

| | | | |
|-----|---|----------------|----------------------------|
| F-1 | TCTATC ^{GCC} _{AGA} A ^G _T GGATGTCT | (245 ~ 265 nt) | 6027 |
| F-2 | TTAGTT ^T _G AA ^{TT} _{AG} TTT ^A _T GT ^T _G T ^A _G GT | (318 ~ 339 nt) | 6028 |
| F-3 | TAGTGTT ^A _G GAG ^T _A A ^G _A GT ^A _G TAAAGA | (346 ~ 368 nt) | 6029 |
| R-1 | A ^A _C TT ^G _A GCCATA ^A _T T ^T _A AACTT | (458 ~ 476 nt) | 6030 |
| R-2 | ACTAA ^{TTAC} _{AATT} T ^G _A G ^C _T ^{GG} _{CT} T ^{AA} _{CC} C ^T _C TAA | (426 ~ 448 nt) | 6031 |
| R-3 | T ^{TG} _{AC} TC ^G _C GC ^{AA} _G T ^{TA} _{GG} C ^{TT} _{CC} C ^C _G GCA | (375 ~ 395 nt) | 6032 6033 |

FIGURE 12

75/193

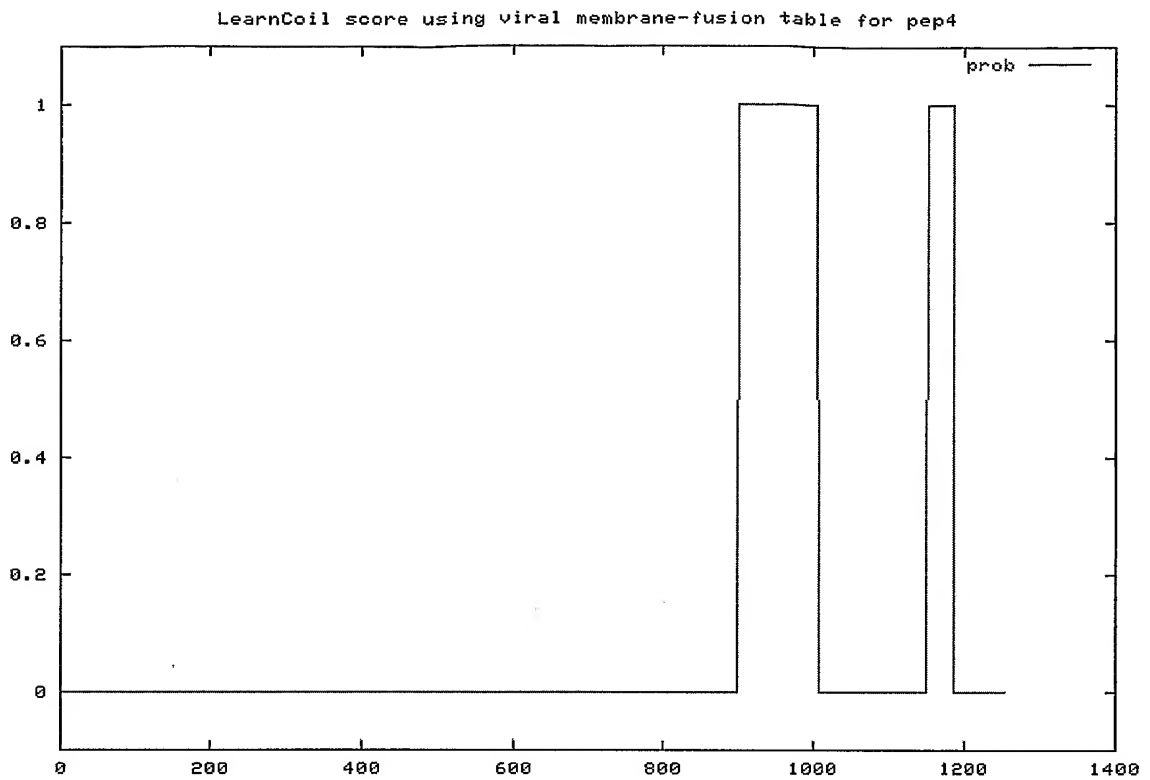
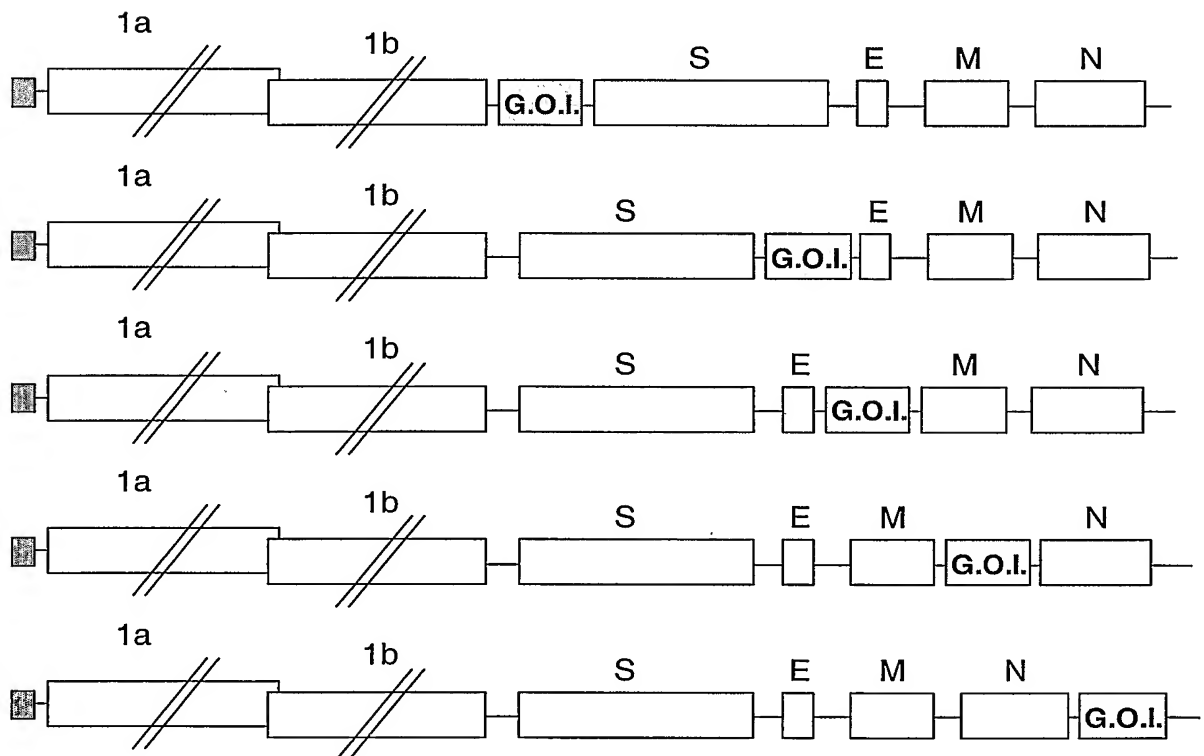
**FIGURE 13**

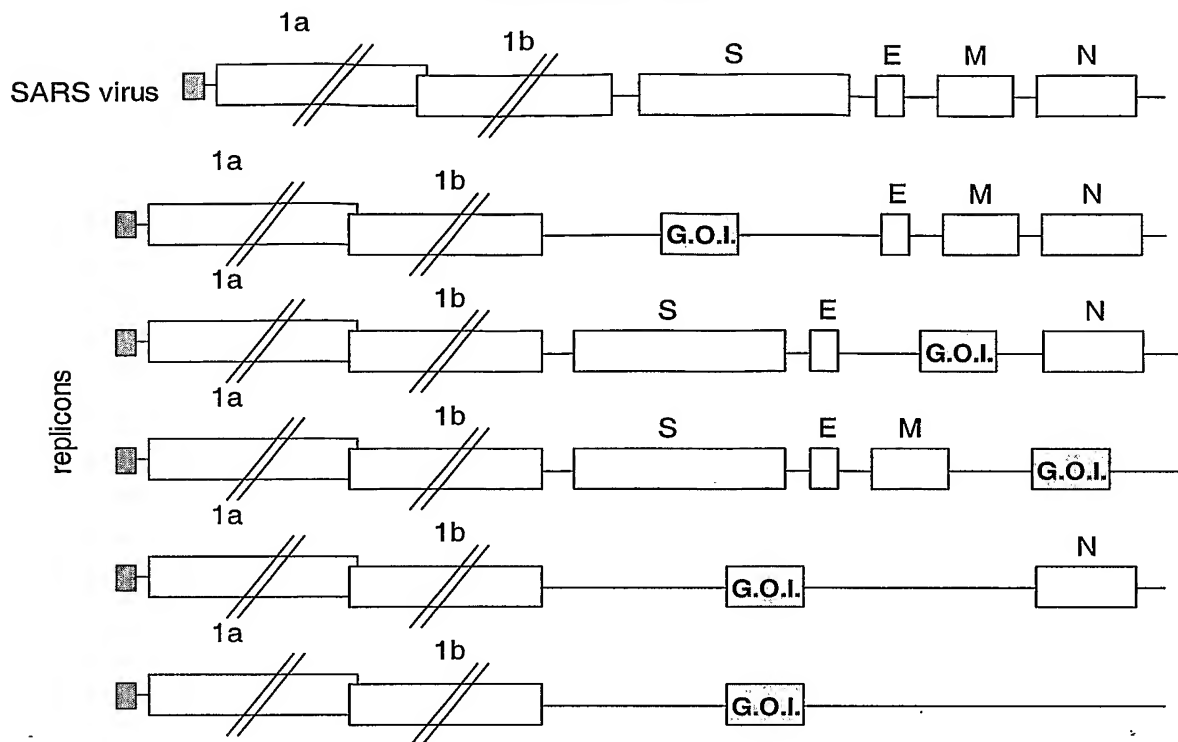
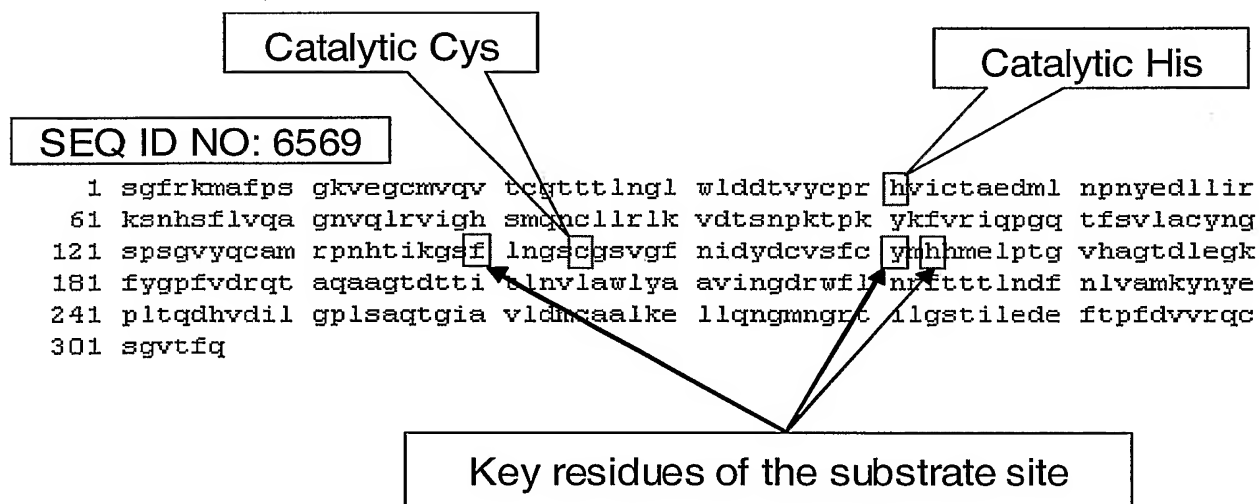
FIGURE 14**FIGURE 15**

FIGURE 16

| Section 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------------|-------|-------------|----------|---------|--------|---------|---------|---------|---------------------|-----------------|------|------|-----|-----|----|----|----|----|----|----|----|---|---|---|---|---|---|----|---|---|---|----|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | (1) | 1 | 10 | 20 | 30 | 40 | 51 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (1) | SGFKALVSPSS | SAVEKCI | SVSVYR | GNNLNL | GLWLGGD | ITTCPR | EVIG--- | KFSG | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (1) | SCIVKMHVSE | PTSKVEPC | IVSVTYG | NMTLNL | GLWLDD | DDKVVCP | RVVICSS | ADMTD | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SARS nsp2 | (1) | SGFRKMAFP | SGKVEGC | IVQVTCG | TTTNG | LWLDD | ITTCPR | RVVIC | TAEDMLN | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| BCoV nsp2 | (1) | SCIVKMHVNP | PTSKVEPC | IVSVTYG | NMTLNL | GLWLDD | DDKVVCP | RVVIC | SSADMTN | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Consensus | (1) | SGIVKMHVSP | SSKVEPC | IVSVTYG | NMTLNL | GLWLDD | DDTVYC | PRHVIC | SAADMTN | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Section 2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (52) | 52 | 60 | 70 | 80 | 90 | 102 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (49) | DQNDV | LNLANNH | FEVTT | QHGVL | LNHV | SRRL | EGAM | LLOQTANANAETPKY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (52) | PDYP | NLLCRVT | SSDFCVM | SGR- | SLTV | MSYQM | QGC | CLVLTVTLQNPNTPKY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SARS nsp2 | (52) | PNYED | LLIRK | NHSFL | VOAGN- | VOLR | YIG | SMQNC | LRLKVDTSNPTPKY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| BCoV nsp2 | (52) | PDYT | NLLCRVT | SSDFTV | FDR- | SLTV | MSYQM | QGC | CLVLTVTLQNSRTPKY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Consensus | (52) | PDY | NLLCRVT | SSDF | VLSGR | VSLTV | MSYQM | QGC | CLVLTVTLQNPKTPKY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Section 3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (103) | 103 | 110 | 120 | 130 | 140 | 153 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (100) | KFIKANCC | DSFTT | ACATGG | TVVGL | PPVTH | RSNGT | IRAS | SLAGACSSVCGNI | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (102) | SFGVV | KPGET | FFTV | LAAYN | GRPQ | GAFHV | TMRSS | HTIKGSLCGSCSSVGVV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SARS nsp2 | (102) | KFVR | IQFGQ | FFSV | LACYN | G | PSGV | YQCAMP | NHTIKGSLNGSCSSVCGNI | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| BCoV nsp2 | (102) | TFGVV | KPGET | FFTV | LAAYN | GKPG | GAHV | TMRSS | HTIKGSLCGSCSSVGVV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Consensus | (103) | KFGVV | KPGET | FFTV | LAAYN | GSPQ | GAFHV | TMRSS | HTIKGSLCGSCSSVGVFI | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Section 4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (154) | 154 | 160 | 170 | 180 | 190 | 204 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (151) | IKGV | VNFF | MHLE | LPLN | ALHT | GTD | LMQ | EFTGGVY | LEEV | AQRV | PPDN | LV | TNN | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (153) | TGDS | V | FV | M | LE | LE | LG | CHT | G | T | D | F | S | C | N | F | Y | C | P | Y | R | L | A | Q | V | Q | L | P | V | Q | D | Y | T | T | O | T | V | N | | | | | | | | | | | | | |
| SARS nsp2 | (153) | YDC | V | S | F | C | M | H | N | E | L | P | T | G | V | H | A | G | T | D | E | C | K | F | T | G | F | V | D | R | Q | T | A | A | A | G | T | D | T | T | I | T | I | N | | | | | | | | |
| BCoV nsp2 | (153) | MGDC | V | K | F | V | M | H | Q | L | E | L | S | T | G | C | H | T | G | T | D | F | N | C | D | F | Y | G | P | Y | K | D | A | Q | V | Q | L | P | V | Q | D | Y | T | T | O | T | V | N | | | | |
| Consensus | (154) | DGDC | V | K | F | V | M | H | Q | L | E | L | S | T | G | C | H | T | G | T | D | L | G | D | F | Y | G | P | Y | V | D | A | Q | V | Q | L | P | V | Q | D | Y | T | T | O | T | V | N | | | | | |
| Section 5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (205) | 205 | 210 | 220 | 230 | 240 | 255 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (202) | VVAW | LYAA | AI | ISV | KESS | FS | SLPK | WLE | STTV | SVDD | YMK | WAG | DNG | GF | PP | FS | TS | -- | T | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (204) | VVAW | LYAA | IF | N | R | C | N | ---- | WFL | QSD | C | S | L | E | D | F | N | W | A | M | S | N | G | F | S | S | I | K | A | D | -- | L | | | | | | | | | | | | | | | | | | | |
| SARS nsp2 | (204) | VVAW | LYAA | I | N | G | D | R | ---- | WFL | N | R | F | T | T | L | E | D | F | N | W | A | M | S | N | G | F | S | S | I | K | A | D | -- | L | | | | | | | | | | | | | | | | | |
| BCoV nsp2 | (204) | VVAW | LYAA | I | N | N | C | N | ---- | WFL | QSD | K | C | S | L | E | D | F | N | W | A | M | S | N | G | F | S | S | I | K | A | D | -- | L | | | | | | | | | | | | | | | | | | |
| Consensus | (205) | VVAW | LYAA | I | I | N | C | N | | WFL | QSD | T | C | S | L | E | D | F | N | W | A | M | S | N | G | F | S | P | I | K | S | D | | L | | | | | | | | | | | | | | | | | | |
| Section 6 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (256) | 256 | 270 | 280 | 290 | 306 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (251) | AT | TKLS | AT | FG | V | D | V | C | K | L | R | T | I | M | V | K | N | S | -Q | GG | D | P | I | L | G | Q | Y | N | F | 3 | D | E | L | T | P | E | S | V | N | N | Q | | | | | | | | | | |
| MHV nsp2 | (247) | V | L | D | A | L | A | S | M | T | G | V | S | L | E | T | L | L | A | A | I | K | R | L | K | N | S | -G | F | Q | G | R | Q | I | L | G | S | C | I | L | E | D | E | L | T | P | S | D | V | Y | Q | Q |
| SARS nsp2 | (249) | V | L | G | P | L | S | A | Q | T | C | T | A | V | L | D | M | C | A | A | I | K | E | L | L | Q | N | G | M | N | A | R | T | I | L | G | S | T | I | L | E | D | E | F | T | R | F | D | V | V | R | Q |
| BCoV nsp2 | (247) | V | L | D | A | L | A | S | M | T | G | V | S | L | E | T | L | L | A | A | I | K | R | L | K | N | S | -G | F | Q | G | R | Q | I | L | G | S | C | S | F | E | D | E | L | T | P | S | D | V | Y | Q | Q |
| Consensus | (256) | V | L | D | A | L | A | A | M | T | G | V | S | L | E | T | L | L | A | A | I | K | R | L | S | G | F | Q | G | R | Q | I | L | G | S | C | I | L | E | D | E | L | T | P | S | D | V | Y | Q | Q | | |
| Section 7 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | (307) | 307 | 313 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| avian IBV nsp2 | (301) | IG | GV | R | L | Q | | | | SEQ ID NO: 6570 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MHV nsp2 | (297) | L | A | G | V | K | L | Q | | SEQ ID NO: 6571 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SARS nsp2 | (300) | C | S | G | V | T | F | Q | | SEQ ID NO: 6569 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| BCoV nsp2 | (297) | L | A | G | V | K | L | Q | | SEQ ID NO: 6572 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Consensus | (307) | L | A | G | V | K | L | Q | | SEQ ID NO: 6573 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

FIGURE 17

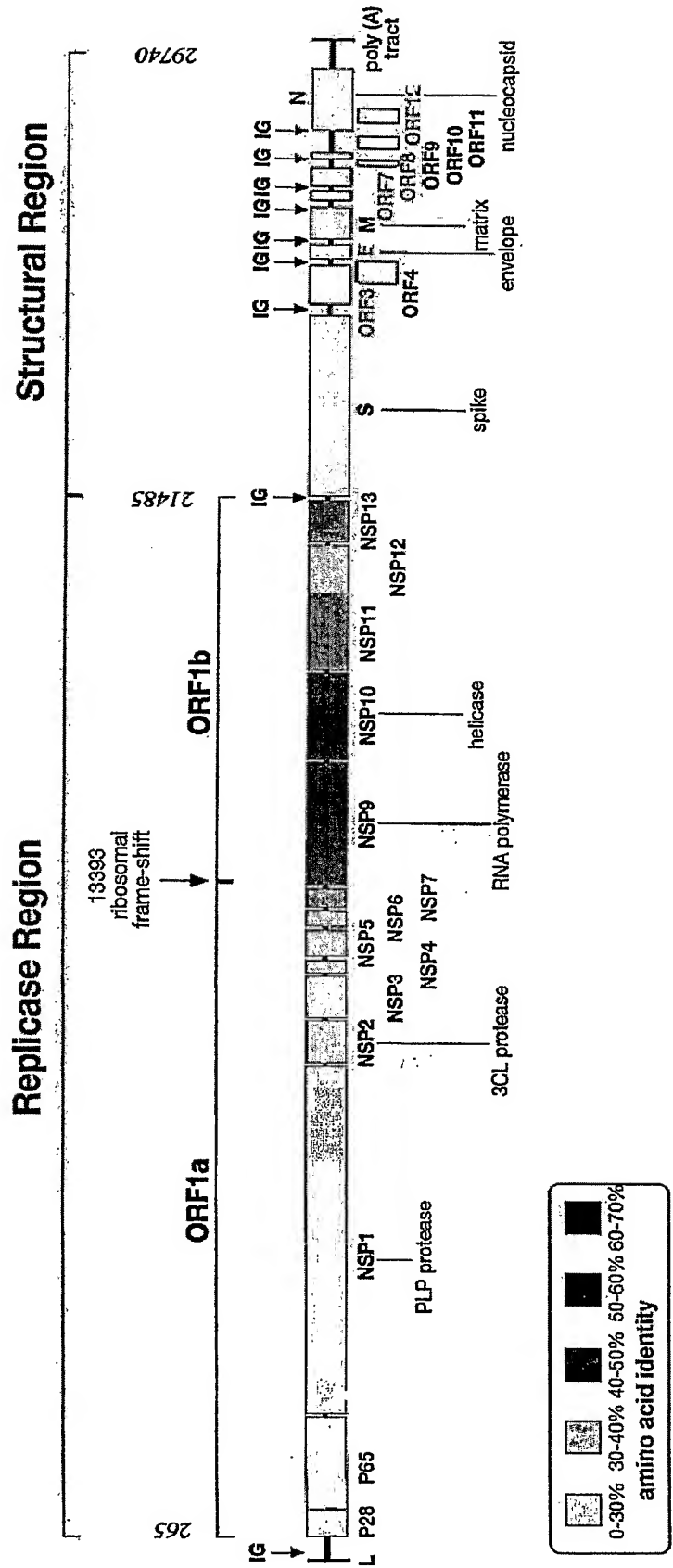


FIGURE 18

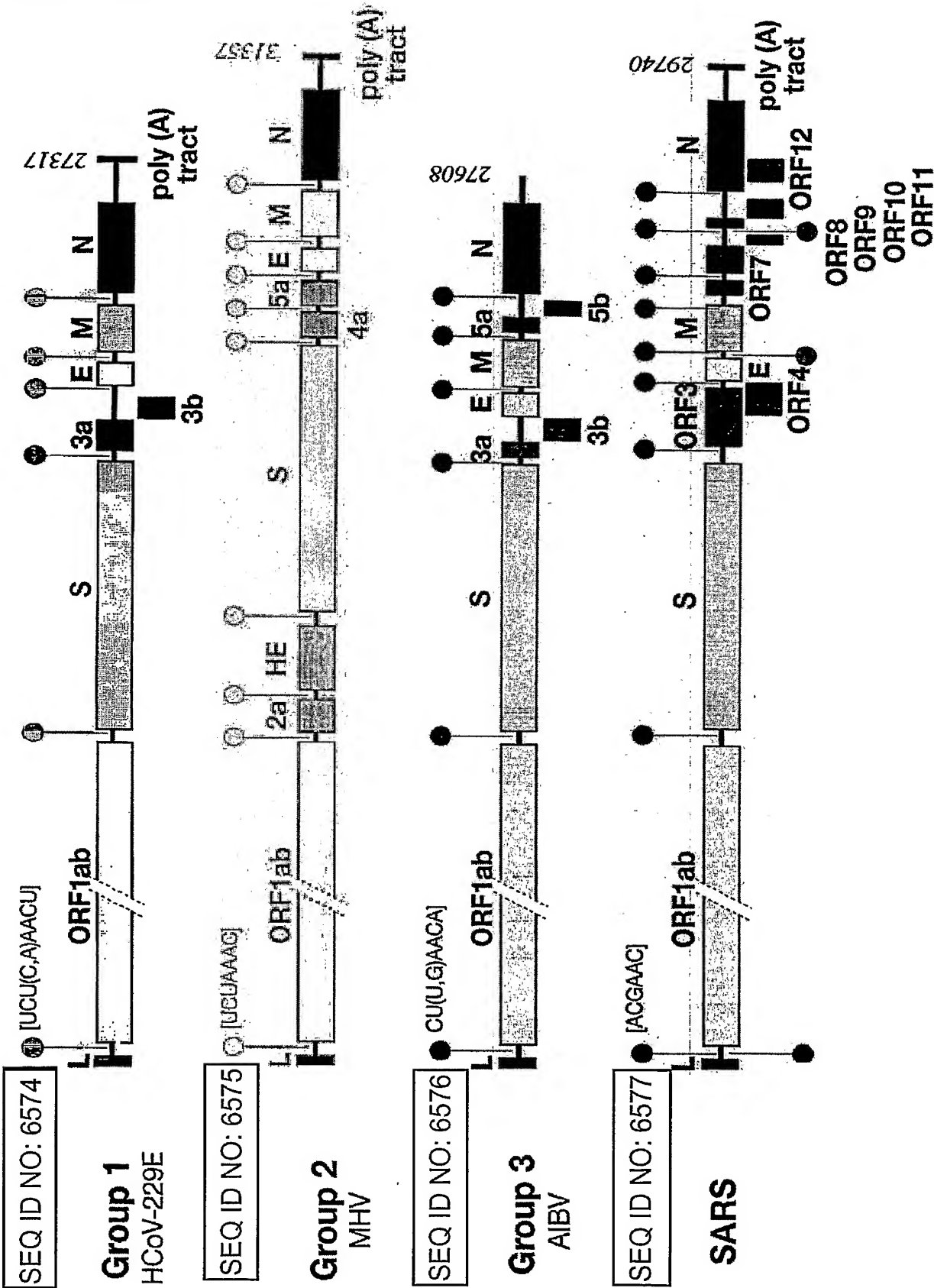


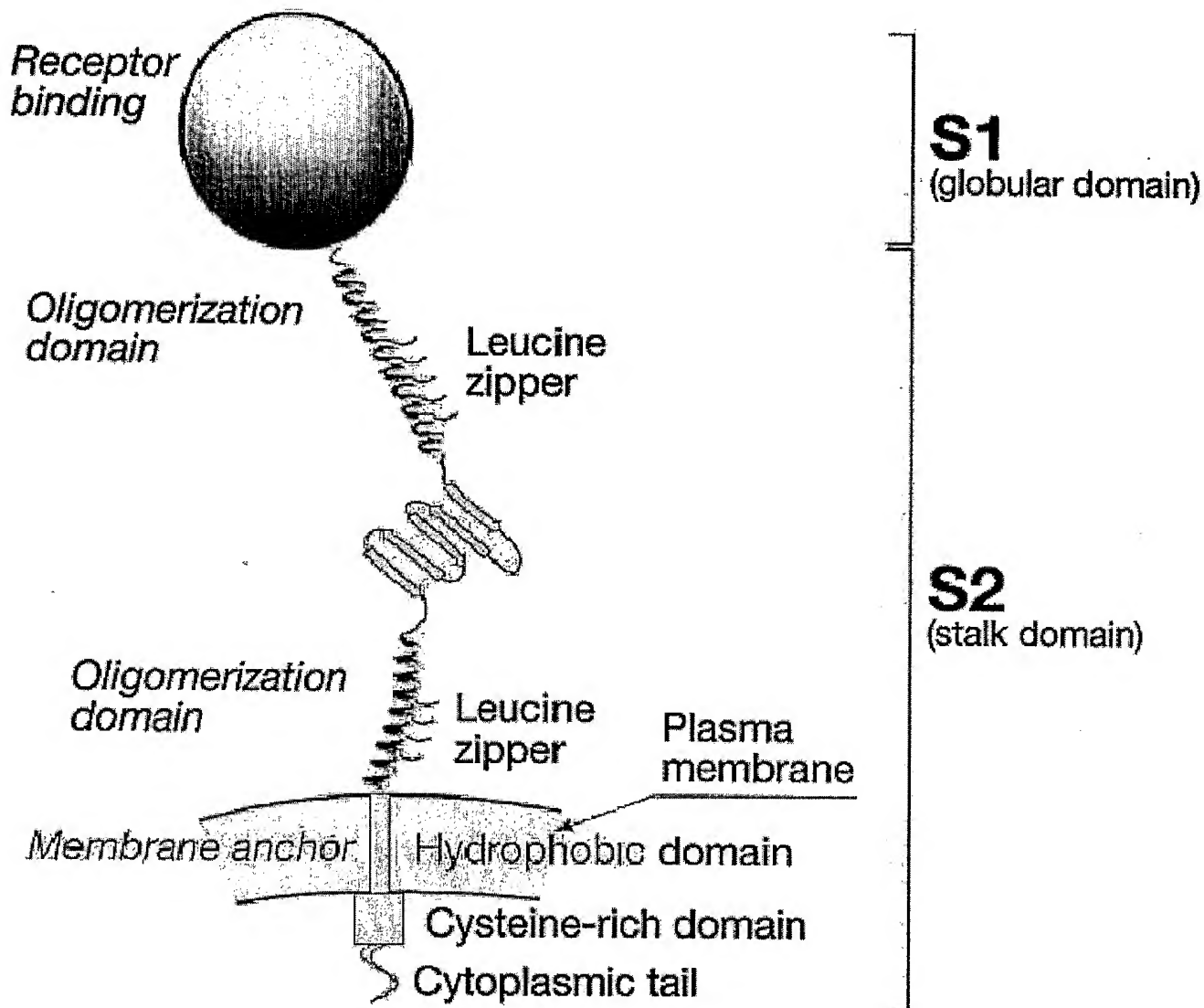
FIGURE 19**FUNCTION****STRUCTURE**

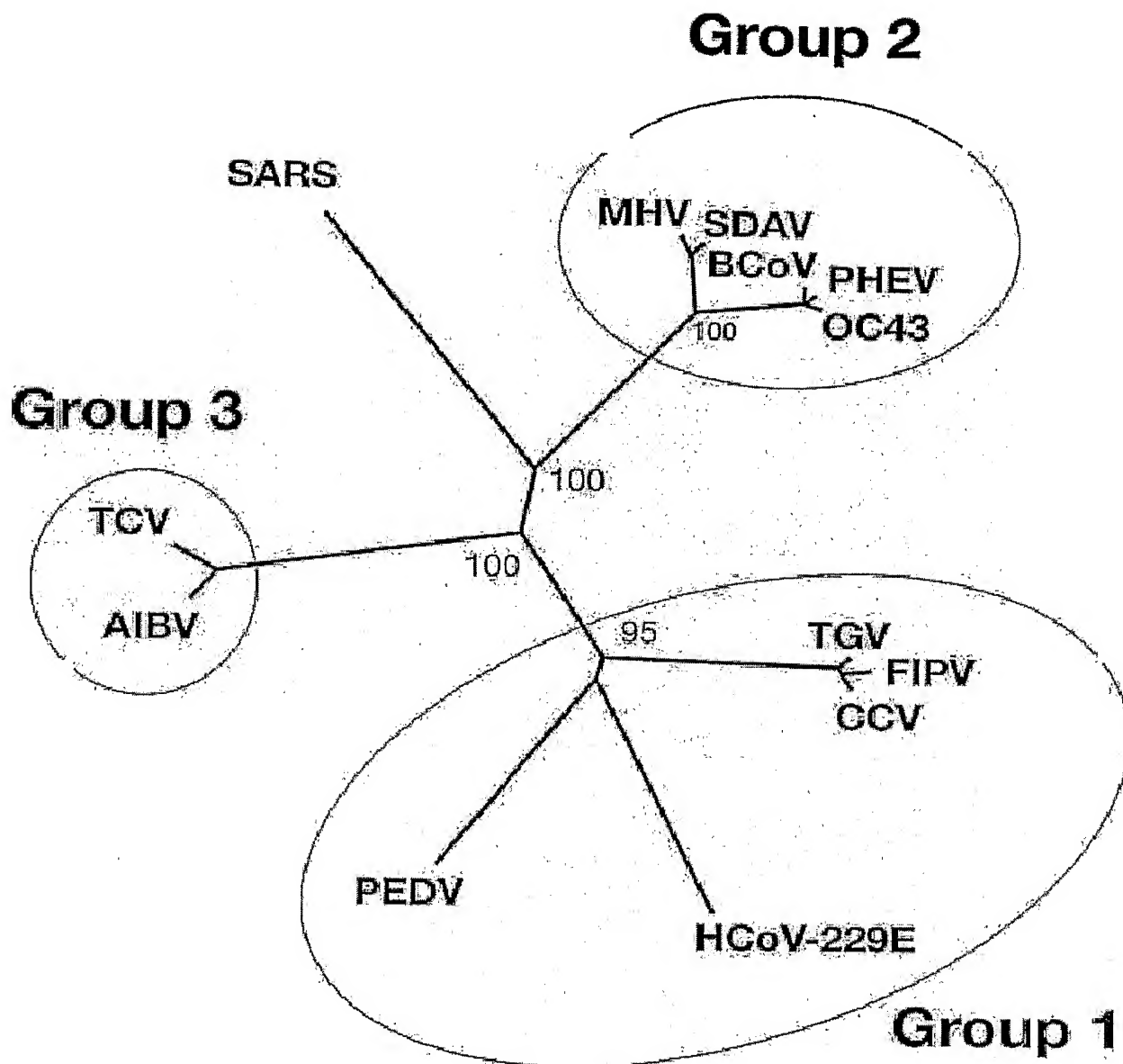
FIGURE 20

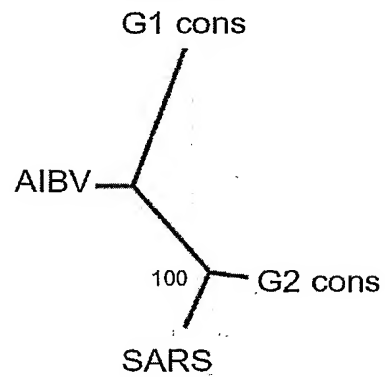
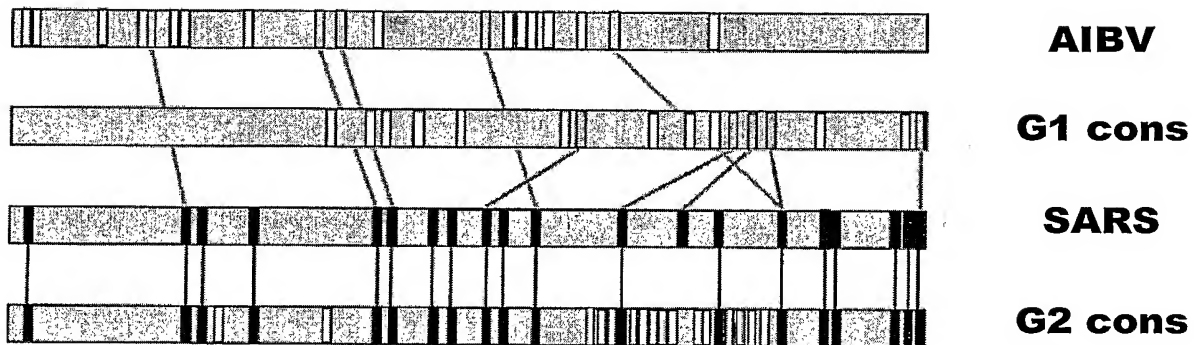
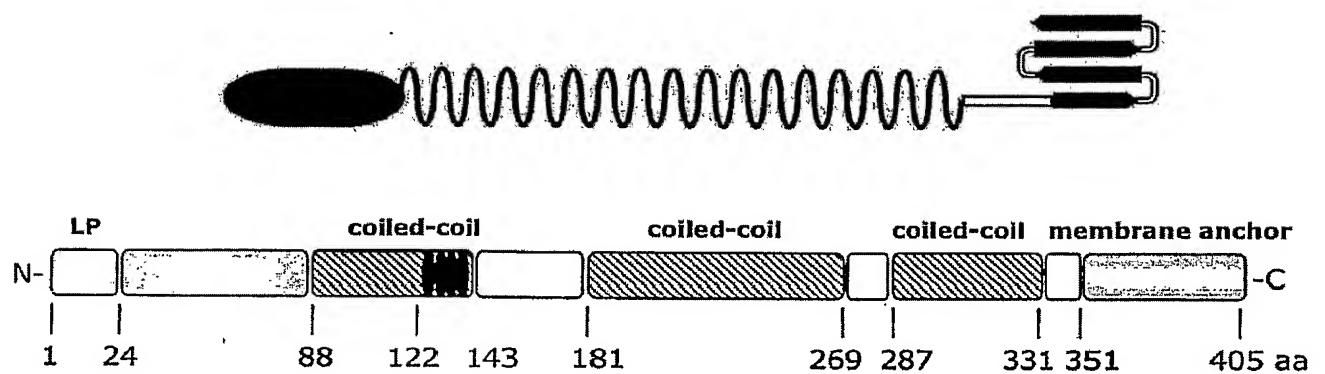
FIGURE 21**FIGURE 21A****FIGURE 21B****FIGURE 22**

FIGURE 23

LPRKSQPTSIISCRSVL-TNFKICVAVARLHA-CTYAV-TIINF TVVDKKRVTRPSSADCL
 RFRPCCSRSSAYLGFVRV-PKGKMESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEE
 ALSEAREHLKNGTCGLVELEKGVLPQLEQPYVFIKRSDALSTNHGHKVVVELVAEMDGIQY
 GRSGITLGLVLPVHVGETPIAYRNVLLRKNGNKGAGGHSYGIDLKSYDLGDELGTDPIDY
 EQNWNTKHGSGALRELTRELNGGAVTRYVDNFCGPDGYPLDCIKDFLARAGKSMCTLSE
 QLDYIESKRGVYCCRDHEHEIAWFTERSDKSYEHQTPFEIKSAKKFDTFKGECPKFVFP
 NSKVKVIQPRVEKKKTEGFMGRIRSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFL
 KATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRL
 RKGGRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDLLEILSRE
 RVNINIVGDFHLNEEVAILASFSASTSFAIDTIKSLDYKSFKTIVESCNGYKVTKGKPV
 KGAWNIGQQRSVLTPLCGFPSQAAGVIRSIFARTLDAANHSIPDLQRAAVTILDGISEQS
 LRLVDAMVYTSDDL TN SVIIMAYVTGGLVQQT SQWLSNLLGTTVEKLRPIFEWIEAKLSA
 GVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVVNKALEMCIDQVTIAG
 AKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTVLTSEEVV
 LKNGELEALETPVDSFTNGAIVGTPVCVNGLMLEIKDKEQYCALSPGLLATNNVFRKLG
 GAPIKGVTFGEDTVWEVQGYKNVRITFELDERVDKVLNEKCSVYTVESGTEVTEFACVVA
 EAVVKTLQPVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYSFYPPDEEEEDDAE
 CEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDETTTEQSEIEPEPEP
 TPEEPVNQFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVAGALNKAT
 NGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGPNLNAGEDIQLLKAAYENFN
 SQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVVM DYLDNLKPRVE
 APKQEEPPNTEDSKTEEKSVVQKPVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADING
 KLYHDSQNMLRGEDMSFLEKDAPYMGDVITSGDITCVVIPSCKAGGTTEMLSRALKKVP
 VDEYITTYPGQGCAGYTLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVSWNLREMLAH
 AEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRRFFFYTSKEPVASIIITKLNSL
 NEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAVVSVSSPDVTTTYNGYLTSSSKTSEEHF
 VETVSLAGSYRDWSYSGQRTTELGVFLKRGDKIVYHTFLES PVEFHLDGEVLSLDKLSLL
 SLREVKTIKVFTTVDNTNLHTQLVDMSMTYGGQFGPTYLDGADVTKIKPHVNHEGKTFV
 LPSDDTLRSEAF EYYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNNCYLSSVL
 LALQQLEVKF NAPALQEAYYRARAGDAANFCALILAYSNKTVGELGDVRETMT HLLQHAN
 LESAKRVLNVVCKHCGQKTTTLTGVEAVMYMGTLSDYDNLKTGVSIPCVCGRDATQYLVQQ
 ESSFVMM SAPP AEYKLQQGTFLCANEYTGNYQCGHYTHITAKETLYRIDGAHLTKMSEYK
 GPVTDVIFYKETS YTTTTIKPVSYKLDGVTYTEIEPKLDGYKKDNAYYTEQPIDLVPQTQPL
 PNASFDNFKLTCSNTKFADDLNQMTGFTK PASRELSVTFFPDLNGDVVAIDYRHYSASF
 KGAKLLHKPIVWHINQATTKTTFKPNTWCLRLWSTKPVDTSNSFEVLAVEDTQGM DNLA
 CESQQPTSEEVENPTIQKEVIECDVKTTTEVVG NVILKPSDEGVKVTQELGHEDLMAAYV
 ENTSITIKKPNELSLALGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRL
 AQRVFNNYMPYVFTLLFQLCTFTKSTNSRIRASLPPTIAKNSVKSVAKLCLDAGINYVKS
 PKFSKLFTIAMWLLLLSICLGLSICVTAAGVLLSNFGAPS YCNGVRELYLNSSNVT TMD
 FCEGSFPCSI CLSGLDSLDSYPALETIQVTISSYKLDLTILGLAAEWV LAYMLFTKFFYL
 LGLSAIMQVFFGYFASHFISNSWLMWFIISIVQMAPVSAMVRMYIFFASFYYIWKSYVHI
 MDGCTSSTCMMCYKRN RATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDTFCT
 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSH
 FVNLDNLRANNTKGSLPINVIVFDGKSKCDESASKSASVYYSQ LMCQPIILLDQALVSDV
 GDSTEVS VKMFDAYVDTF SATFSVPMEKLKALVATAHSELAKGVALDGVLSTFVSAARQG
 VVDTDVDTKDVIECLKLSHSDLEVTDGSCNNFMLTYNKVENMTPRDLGACIDCNARHIN
 AQVAKSHNVSLIWNVKDYMSLSEQLRKQIRSAAKNNIPFRLTCATTRQVNVNITTKISL
 KGGKIVSTCFKLMLKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDI
 ISTDDCFANKHAGFDWFSQRGGSYKNDKSCP VVAIIITREIGFIVPGLPGTVLRAIN GD
 FLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAAECTIFKDAMGKVPYCYDTNLL E
 GSISYSELRPDTRYVLMDGSIIQFPNTYLEGSVRVVTTFDAEYCRHGT CERSEVGICLST
 SGRWVLNNEHYRALSGVFCGVDAMNLIANIFTPLVQPVGALDVSASV VAGGIIAILVTCA
 AYYFMKFRRVFGEYNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDV
 SFLAHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLRKRVMFNGVTFSTFE EAL

CTFLLNKEMYLKLRSETLLPLTQYNRYLALYNKYKYFSGALDTTTSYREAACCHLAKALND
FNSNGADVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTTTLNGLWLDDTVY
CPRHVICTAEDMLNPNYEDLLIRKSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPK
TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNHTIKGSFLNGSCGSGVGFNIDYDCV
SFCYMHMELPTGVHAGTDLEGKFYGPFDVDRQTAQAAGTDTTITLNVLAWLYAAVINGDR
WFLNRFTTTLNDFNLVAMKYNIEPLTQDHVDILGPLSAQTGIAVLDMCAALKELLQNGMN
GRTILGSTILEDEFTPFDDVVRQCSGVTFQKGFKKIVKGTHHWMLLTFLTSLILVQSTQW
SLFFFVYENAFLEPFTLGIMAIAACAMLLVKHKHAFCLCLLPLSLATVAYFNMVYMPASWV
MRIMTWLELADTSLSGYRLKDCVMYASALVLLILMTARTVYDDAARRVWTLNMVITLVYK
VYYGNALDQAI SMWALVISVTSNYSYSGVVTTIMFLARAI VFCVEYYPLLFITGNTLQCIM
LVYCFGLGYCCCCYFGLFCLLNRYFRLTLGVYDYLVSSTQEFYRMYNSQGLLPKSSIDAFKL
NIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSSKLWAQCVQLHNDILL
AKDTTEAFEFKMSVLLSVLLSMQGAVDINRLCEEMLDNRATLQAIASEFSSLPSYAAAYATA
QEAYEQAVANGDSEVVLKKLKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSED
KRAKVTSAMQTMLEFMTLRKLDNDALNNIINNARDGCVPLNIIPLTTAAKLMVVVPDYGT
KNTCDGNTFTYASALWEIQQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANSVAVKLQ
NNELSPVALRQMSCAAGTTQTACTDDNALAYNNSKGGFRVLALLSDHQDLKWARFPKSD
GTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGLNNLNRGMVGLSLAATVRLQAGNATEV
PANSTVLSFCFAVADPAKAYKDYLASGGQPTNCVKMLCTHTGTGQAITVTPEANMDQES
FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVCGMWKGYG
CSCDQLREPLMQSADASTFLNGFAV-VQPVLHRAAQALVLMSSSTGLLIFTTKKLLVLQSS
-KLIASVRRMRKAIY-TLTL-LRGILCLTTNMKRLFITWLKIVQRLLSMTFSSLE-MV
TWYHIYHVS-VNTQWLI-SMLYVILMRVIVIH-KKYSSHTIAVMMIISIRRIGMTS-RI
LTSYAYMLT-VSVYANHY-RLYNSAMLCVMQAL-AY-H-IIRILMGTGTISVISYK-HQA
AEFLLEWIIHITHC-CPSSL-LGHWLLSPIWMLISQNHLLSGIC-NMILRKRDFVSSTVILN
IGTRHTIPIVLTVMIGVSFIVQTLMCYFLLCFHLQVLDH--EKYL-MVFLLLFQLDTIF
VS-ESYIIRM-TYIARVSVS RNFCMLLIQLCMQLLAIYC-INALHAFQ-LH-QTMLLFK
LSNPVILIKTFMTLLCLKVSLRKEVLLN-NTSSLLRMATLLSVIMTIIVIIICQQCVISDN
SYS-LKLLINTLIVTMVAVLMPTK-SLTIWINQLVSHLINGVRLDFIMTQ-VMRIKMHFS
RILSVMSLL-LK-ILSMPLVQRIELAP-LVSLSVVL-QIDSFIRNY-SQ-PPLEELLW-
LEQASFTVAGIIC-KLFTVM-KLHTLWVGIIQNVTEPCLTCLG-WPLLFLLANITLAVTY
HTVSTG-LTSVRKY-VRWSCVAAHYMLNQVEHHPVMLQLLMLIVSLTFVKLLQPM-MHFF
QLMVIR-LTSMIAIYNTGSMVSIEIGMLIMNSWMSFTLTVCVNISP--FFLMPLCAITV
TMRLKV--LALRTLROFFIIKIMCSCLRQNVGLRLTLLKDLTNFAHSIQC-LNKEMITCT
CLTQIHQYEQ-AQAVLSMILSKQMVHL-LKGSCHWLLMLTHLQNILIRSMMSFTCIYNTL
ESYMSLLATCWTICIP-C-LMITPHGTGNLSFMRLCTHHIQSCRL-VLVYCAIHRHFVA
VPVLGDHSYVASAAMTMSFQHHTN-CCLLIPMFAMPQVVMSSLM-HNCI-EV-AIIASHIS
LPLVFHYVLMVRFLVYTKTHV-AVTMSLTSMR-QHVI GLMLAITYLPTLVLRDSSFSQOK
RSKPLRKHLSCHMVLPLYAKYSLTENCIFHGRLENLDHH-TETMSLLVTV-LKIVKYRLE
STPLKKVTMVMLLCTEVLRLHS-MLVITLC-HLTL-CHLVHLL-CHKSTM-ELLACTQHS
TSQMSFLAMLQIIKRSACKSTLHSHKDLVLVVRVILPSDLLSITHLLA-CIRHALMQLLMP
YVKRH-NICP-INVVESYLRVRA-SVLINSK-IQH-NSMFSAI-MHCQKQLLTL-SLMKS
LWLLIMT-VLSMLDFVQNTTSILAILLNYQPPAHC-LKAH-NQNILIQCADL-KQ-VQTC
SLELVAVVLLKLLTL-VL-FMTIS-KHTRISQLNASKCSTKVLLHMMFHLQSTD LK-AL-
ENFLHAILLGEKLFSLHLLIHRTL-LQKS-DCLRLLIHRVNLMTMSYSHKLLKQHTLV
MSTASMWLSQGQKLAFC-CLIEIFMTNCNLQV-KYHVAMWLHYKQKM-LDFLRTVVRSL
LVFILHRHLHTSALI-SSRLKDYVLTYQAYQRT-PTVDSSL-WVSK-ITKSMVTLICLSP
AKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPE
LMQNLHQVTSNLILYHSCIKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALSLHQ-
STLSRLDLKERVVCVTNVQLAFLHQLIMPAGIILWVLTMSITHL-LMFSSGALRVTFRV
TMTNIARYMEMHMLVVMML-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTW
L-SLHCLLISFQFFMTLEIQRLLSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILMLHITI
NSLMVFVFCGIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVVC-ISMHSTLQLSIKVH
LLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQMSTDSTW
MHII--FLDLAYGFTNNLILITCGIHLPGYRV-KMWLIMLLIKDTLMDTPAKHLFPSLI
MLFTQR-MVLMWRSCLKIRQHFLMLHLSFGLSVTLNQCQRLRYSIWVLISLLIL-SGTT

KEKPQHMYLQ-VSAQ-LTLPRNLLRVLVLHLLSCLMVWVKDR-TFLETPVMVF--QKVQS
KV-HLQORDQHKLASMESH-LENQ-KHSLTTLRK-TALFNSCLKPTLLRAET-RILSPDHK
WKLTFSSSLWMNSYSDISSRAMPSNTSFMEISVMDNLAVFI---A-PSAHKIHHLN-RIL
SLWTAQ-KITS-QMRKQVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFH
SCFGVRMDMLKPSTQNYKQVERGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE---
MSQSILNCVNT-IHLL-LYPTT-ELFTLVLALIKELHQVQLCSDNGCQLAHYLSIQILMT
SSPTHILL-LETVQQYIRLINGTLLLAICMTLGPNM-QKRMTLKKGFSLICVDL-SKN-P
WVVL-L-R-QSILGMLTFTSLWAI SHGGQLLQOM-MHHHRKHF-LGLTILASRRNKLMAI
PCMLTTFSGGTQILSSCLPIHSLT-ANFLN-EELL-CLLRRIKSMI-FILFWKKVGLSL
EKTTELWFQVIFLLTTKRTCLFSYYFLLSLVVVTLTGAPLLMMFKLLITLNLHL-GGFT
ILMKFLDQTLFI-LRIYFFHFILMLQGFILLIIRLATLSYLLRMVFIILLPQRNQMLS SVVG
FLVLP-TTSHSR-LLLTILLMLLYEHVTLNVCVTTL SLLFLNPWVHRHIL-YSIMHLIALS
STYLMPPFRMLFQKSQVILNTYESLCLKIKMGFSMFIRAINL-M-FVIYLLVLT-LNFLS
CLLVLTQLILEPFLQPFHLLKTFGARQLQPILLAI-SQLHLCSSMMKMVQSQMLLIVLKI
HLLNSNALLRALRLTKEFTRPLISGLFPQEML-DSLILQTCVLLERFLMLLNSLLSMHGR
EKKFLIVLLITLCSTTQHFFQPLSAMAFLPLS-MIFASPMQMILL-SREMM-DK-RQDK
LVLLLI I I I INCQMISWVVSLLGILGTLMMLLQLVII I I INIGILDMASLGPLRETYLMCLSP
LMANLAPHLLLLIVIGH-MIMVFTPLLALATNLTEL-YFLLNF-MHRPRFVDQNYPLTLLR
TSVSILILMDSLVLVC-LLLQORDFNHFNNLAVMFLISLIPFEILKHLKY-TFHLALLGV-
V-LHLEQMLHLKLLFYIKMLTALMFLQQFMQINSHQLGAYILLETMYSRLKQAVL-ELSM
STLLMSATFLELAFVLVTIQFLYVVLAKNLLWLILCL-VLIVQLLTLITPLLYLLTFQ
LALLQK-CLFLWLKPP-IVICTSAEILLNVLICFSNMVAFAHN-IVHSQVLLLNRIATHV
KCSLKS NKCTKPQL-NILVVLIFHKYYLTL-SQLRGLLLRTCSLIR-HSLMLAS-SNMAN
A-VILMLEISFVRRSSMDLQCCHLCSLMI-LLPTLLL-LVVLPLLDGHLVLALLFKYLLL
CKWHIGSMALELPKMF SMRTKNKSPTNLTRRLVKFKNHLQQHQLHWASCKTLLTRMLKH-
THLLNNLALILVQFQVC-MISFRDLIKSRRRYKLTG-LQADFKAFKPM-HNN-SGLLKSG
LLLILLLLKCLSVFLDNQKELTFVERATTLCPSHKQPRMVLSSYMSRMCHPRRGTS PQRQ
QFVMKAKHTSLVKVFLCCLMALLGLLHRGTSFLHK-LLQTIHLSQEIVMSLLASLTQFMI
LCNLSLTHSKKSWTSTSKI IHHQMLILATFQALTLLSSTFKKKLTASMRSLKI-MNHSLT
FKNWENMSNINLGLGMFGSASLLD-LPSSWLQSCFVA-LVVAVASRVHALVVLAASLMRM
TLSQFSRVSNYITHKRTYGFVYEIFYSWINYCTASKN-QCFSCKYCSCYSNDTATSLTPF
RMACYWRCISCCFSERYQNNCAQ-KMAASPL-GLPVHLQFTAAICYHLFTSFACRCRYGG
AIFVPLCLDIFSTMHORM-NYYEMLALLEVQIQEPITL-CQLLCLLAHT-L-LLYTI-QC
HRYNCRY-R-RHFNTKTQRRLPNWWLF-G-ALRC-RLCRCTWLFHRSLLPA-VYTNYYRH
WY-KCYILHL-QAC-RPTECANTHNRRLFRSC-SSNGSNL--ADDDY-RAFVSTRK-VRT
YVLIRFGRNRYVNS--RTSFSCFRGILASHTSHPYCASIVCVLLQYC-REFSKTNGLRLL
AC-KSELF-RSS-SSGLNELTII I I I LFGTLTLLIMADNGTITVEELKQLLEQWNLVIGFL
FLAWIMLLQFAYSNNRNLFLYII I I I KLVLFWLLWPVTLACFVLA AVYRINWVTGGIAIAMACI
VGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLRGITVTRPLMESELVIGAVIIRG
HLRMAGHSLGRCDIKDLPKEITVATSRTLSYYKLGASQRVGTD SGFAAYNRYRIGNYKLN
TDHAGSNDNIALLVQ-VTTDVSSC-LPGYNSRDIDYHYEDFQDCYLES-RYNKFNSETII
-ASN-EELFGVR--RTYGVRLSIKRT-KLFSS-H-LYLHLASYITIRSVLEVRLYY-KNL
AHQEHTRAIHFTLLLTINLH-LALAHTLLLLVLTVLDIPISCVQDQFHQNFSSDKRRFN
KSSTRHFFSLLLL-YF-YFASPLRERQNE-AHFN-LLFVLFSLSAIPCFNNAYYILVFTR
NPGSRRTLYQSLNEHETSHCFDLYFSMQLHMHCSALCI--TSCA-RSL-GTTLGVLILIA
LLGFVL-ERFYLFIDGTLWFKHAHMLLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLL
F-INEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQNGRNGARPKQRRPQGLPNNTAS
WFTALTQHGKEELRFPRGQGVPI NTNSGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFY
YLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVQLPQGTTL PKGF
YAEGSRGGSQASSRSSRSRSGNSRNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLE
SKVSGKGQQQQGQTVTKKSAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDL
IRQGTDYKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVI
LLNKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLPAADMDDFSRQLQNSM
SGASADSTQA-TLMMTTQGRWAM-TFSQFRLRYIVYSCAE-ILVTKQHK-V-LTLISHSN
L-SMCNIREDLKEPPHFHRGHAEYDRGYSE-C-GELPIWKSPNV-N-F-CYPHVILIAS

FIGURE 24

TQEKPTNLDLL-ICSLNEL-NLCSCRSAACLVHLRSINNNKFYCR-QETSNSSLFCRLLT
VSSVLQSIISIPRFRPGVTER-DGEPCSWCQRENTTRPTQFACPSG-RRASAWLRGLCGRG
PIGGT-TPQKWLWSSRAGKRRTAPA-TALCVH-TF-CLKHQSRPQGR-AGCRNGRHSVR
S-RYNTGSTRATCGRNPNCIPQCSSS-ER--GSRWS-LWHRSKVL-LR-RAWH-SH-RL-
TKLEH-AWQWCTP-THS-AQWRCSHSLCRQQFLWPRWVPS-LHQRFSTRTRGQVNVHSFRT
T-LHRVEERCLLLLP-P-A-NCLVH-AL--ELRAPDTRLN-ECQEI-HFQRGMPKVCVSS-
LKSQSHSTTC-KEKD-GFHGAYTLCVPCCISTGV-QYALVYLDLDEM-SLR-SFMADVRLSE
SHL-TLWH-KFSY-RTYYMWVPTY-CCSENAMSCLSRPRDWT-A-CCRLSQPLKH-NSTP
QGR-D-MFWRLCVCLCWLL--ACLLGSSC-C-YWLRPYWHYW-QCGDLE-GSP-DTES-T
C-H-HCWRFSE-EGCHHFGIFLCFYKCLY-HYKES-LQVFQNH-C-VLR-L-SYQGKARK
RCLEHWTTEISFNTTVWFSLTGCWCYQINFCALT-CSKPLNS-FAKSSCHHT-WYF-TVI
TSCRRHGLYFRPAHQQCHYYGICNWWSCCTTDFSVVV-SFGHYC-KTQAYL-MD-GET-CR
S-ISQGCGLGDSQISHYRCF-HRQGSNTGCFR-HQGLCKMLH-CC-QGTRNVH-SSHRYWR
KVAITQLR-SLHRSKQGTLPVYTWQGAATTHAS-GTKRSNLS-R-FT-HSTYL-GGCS
QER-TRSTRDAR--LHKWSYRRHTSLCKWPHALRD-GQRTILRIVSWFTGYKQCLSLKRG
CTN-RCNLWRRYCLGSSRLQECENHI-A--TC-QSA--KVLCLHC-IRYRSY-VCMCSSR
GCCEDFTTSF-SPYQHGYS--VECSYILLI--CW-RKLFITYVLFLLPSR-GRRGRCRV
-GRN--NL-T-VRYRG-LSRSPSGIWCLS-NSSS-GRRRGRLAG-YY-AIRD-ARTRTY
T-RTS-SVYWLFKTY-QCCH-MC-HR-GGTKC-SYGDCKCC-HTPETWWWCSRCTQQGNQ
WCHAKGE--LH-AKWPSYSRRVLFAPWT-SC-EVSACCWT-PKCR-GHPAS-GSI-KFQF
TGHLTCTIVSRHIWC-TTSVFTSVRADGSYTGLYCSQ-QSSL-AGCHGLS--PEA-SGS
T-TRGATKHRRFQ-GEICRTEACRCEAKN-GLH--GYHNTGRN-VSYQ-VTLVC-YQW-
ALP-FSEHA-R-RYVFP-EGCTLHGR-CYH-W-YHLCCNTLQKGWWHY-DALKSFEEAS
--VYNHVPWTRMCWLYT-GS-DCS-EMQICILCTTFRST-C-GRDSRNCILEFERNACSC
-RDKKINAYMHGC-SHNGNHPT-V-RN-NSRGHR-LWCPILLY--RACSFYYYEAEISK
-AACHNANWLCDTWF-S-RGCALYAFS-SSCRSVSIITRCCYYI-WIPHFVIKDI-GALC
RNSFFGWLLQRLVLFRTAYRVRC-IS-AW-QNCVPHSGEPRRVSS-R-GSFT-QTKESLI
PAGG-DYKSVHNCGQH-SPHTACGYVYDIWTAVWSNILGWC-CYKN-TSCKS-G-DFLCT
T--HTT--SFRVLPYS--EFSW-VHVCFKPHKEMEISSSWWFNFN-MG--QLLFV-CFI
STSTA-SQIQCTSTSRGLL-SPCW-CC-LLCTHTRLQ--NCWRAW-CQRNYDPSSTAC-F
GICKASS-CGV-TLWSENYLNGCRSCDVYGYSL--S-DRCFHSMCVWS-CYTISSTTR
VFFCYDVCTTC-V-ITARYILMCE-VHW-LSVWSLHSYCN-GDPLSY-RSSPYKDVRVQR
TSD-CFLQGNILHYNHQACVV-TRWSYLHRD-TKIGWVL-KG-CLLYRAAYRPCTNSTIT
KCEF--FQTHMF-HKIC--FKSNDRLHKASFTRAICHILPRLEWRCSGY-L-TLFSEFQE
RC-ITA-ANCLAH-PGYNQDNVQTKHLVFTLSLEYKASRYFKFI-SSGSRHTRNGQSC
-KSTTHL-RSSGKSYHTEGSHRV-RENYRSCRQCHT-TIR-RC-SNTRVRS-GSYGCLCG
KHKHYH-ET--AFTSLRFKNNCHSWYCCN--CSLE-NFGLCQTLIRTSNNYNIKL-R-EIS
TTCV-QLYALCVYIIVPIVYFY-KYQF-N-SFTTYNYC-K-C-ECC-IMFGCRH-LCEVT
QIF-IVHNRYVAIVVKYLLRFSNLCNCCFWCTLI-FWCSFLL-WR-RIVS-FV-RYYYGF
L-RFFSLQHLFKWIRLP-FLSSS-NHSGDDFIVQARLDNFRSGR-VGFGIYVVKILLFI
RSFSYNAGVLWLFC-SFHQQFLAHVVYH-YCTNGTRFCNG-DVHLLCFLLHMEELCSYH
GWLHLFDLHDVL-AQSCHTR-VYNYC-WHEEIFLCLCKWRPWLLQDSQLELSQL-HILHW
-YIH--SCS-FVTPV-KTNQPY-PVIVYC--CCCEKWRASPLL-QGWSKDL-ETSALPF
CQFRQFES-QH-RFTAY-CHSF-WQVQMRVCF-VCFCVLQSAADVPTYSA-PSSCIRRW
R-Y-SFR-DV-CLCRHLFSNF-CSYGKT-GTCCYSSQRVSKGCSFRWCIFYIRVSCPTRC
C-YRC-HKGCY-MSQTFTSL-LRSDR-QL-QFHAHL--G-KHDAQRSWRMY-L-CKAYQC
PSSKKSQCFTHLECKRLHVFI-TAA-TNS-CCQEEQHTF-TNLCYN-TGCQCHNY-NLTQ
GW-DC-YLF-TYA-GHIIVRSCCIGLLYRYASTYIVNP-WLHK-NHWLQSHSGWCHS-HH
FY--LFCK-TCWF-RMV-PAWWFIQK-QKLPCSSCYHYKRDWFHSAWLTGYCAESNQW-L
LAFSTSCF-CCWQHLLHTFQTH-V--FCYLCLRSSC-VYNF-GCYGQTCAILL-H-FARG
FYFL--ASSRHSLCAYGWFHHTVS-HLPGGFC-SSNNF-C-VL-TWYMRKVRSRYLPIYQ
W-MGS--ALQSSIRSFLWC-CDESHS-HLYSSCATCGCFRCVCFSSGWYCHIGDLCC
LLLYEIQTCTFW-VQPCCC-CTFVFDVFHYTSLSGTSLQLSAGSLLSLLLVLDILFHQ-CF
ILGSPSMVCHVFSYCAFLDNSNLCILYFSEALPLVL-QLS-EKSHV-WSYI-YLRGGCFV

YLFAQQGNVPKIA-RDTVATYTV-QVSCSI-QVQVFQWSLRYQLS-SSLLPLSKGSK-L
-QLRC-CSLPTTTDINHFCSSAEWF-ENGIPVRQS-RVHGTSNLWNYNNS-WIVVG-HSIL
SKTCHLHSRRA-S-L-RSAHSQIQP-LSCSGWQCSTSCYWPFIYAKLSA-A-S-YF-P-D
TQV-ICPYPTWSNIFSSSMLQWFTIWCLSVCHET-SYH-RFFP-WIMW-CWF-H-L-LRV
FLLYASYGASNRSTRWY-LRR-ILWSIC-QTNCTGCRYRHNHNIKCFGMAVCCCYQW--V
VS--IHHYFE-L-PCGNEVQL-TFDTRSC-HIGTSFCSNRNCRRLRYVCCFERAAAEWYEW
SYYPW-HYFRR-VYTI-CC-TMLWCYLPR-VQENC-GHSSLDAFNFLDITIDSCSKYTVV
TVFLCLRECFLAIYSWYYGNCCMCYAC-A-ARILVLVSVTFSCNSCLL-YGLHAC-LGD
AYHDM-A-IG-H-LVWL-A-GLCYVCFSSFSFAYSHDSSHCL--CC-TCLDTDECHYTCLQS
LLW-CFRSSYFHVGLSYFCNL-LFWCRYDYHVS-SYSVCVC-VLPIVIYYWQHLTVYHA
CLLFLRLLLLLLLLPFLFTQPLLQAYSWCL-LLGLYTRI-VYELPGAFAS-E-Y-CFQA-
H-VVGYWR-TMYQGCYCTV-NV-RKVHICGTALGSST-SRVIF-IVGTMCTTPQ-YSSC
KRHN-SFREDGFSFVCFAIHAGCCRH--VVRGNAR-PCYSSGYCFRI-FFTIIICRLCHCP
GGL-AGCS-W-F-SRSQKVKEIFECG-I-V-P-CCHATQVGKDGSRGYDPNVQTGKI-GQ
EGKSN-CYANNALHYA-EA---CT-QHYQQA-WLCSTQHHTIDYSSQTHGCCP-LWYLQ
EHL-W-HLYICICTLGNPASC-CG-QDCST--N-HGQFTKFGLASICYSSKSQLS-CTE
--TESSSTTTDVLGCGWYHTNSLY--QCTCLL-QFEGR-VCAGITIRPPRSQMG-IP-E-W
YRYNLHRTGTTL-VCYRHTKRA-SEILVLHQRLKQPK-RYGAGQFSCYSTSSGWKCYRST
CQFNCAFLLCFCSRPC-SI-GLPSKWRTTNHQLCEDVVYTHWYRTGNYCNTRS-HGPRVL
WWCFMLSVL-MPH-PSKS-RIL-LER-VRPNTYHLC--PSGFYT-KHSLYRLRNVERLWL
-L-PTPRTLDVCGCINVFKRVCVSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFL
KTNCCRFQEKDEEGNLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFKFRVDGD
MVPHISRQRLTKYTMADLVYALRHFDDEGNCDTLKEILVTYNCCDDDYFNKKDWYDFVENP
DILRVYANLGERVRQSLKTVQFCDAMRDAGIVGVLTLDNQDLNGNWDYDFGDFVQVAPGC
GVPIVDSYYSLLMPILTLTRALAAESHMDADLAKPLIKWDLKDYDFTEERLCLFDRYFKY
WDQTYHPNCINCLDDRCILHCANFNVLFTSTVFPTSFGLVLRKIFVDGVPFVSTGYHFR
ELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNVAFQT
VKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYRYNLPTMCDIRQL
LFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKKGKARLYYDSMSYEDQDALFA
YTKRNVIPITITQMNLYAISAKNRARTVAGVSICSTMTNRQFHQKLLKSIAATRGTATVVI
GTSKFYGGWHNMLKTVYSDVETPHLMGWDYPKCDRAMPNMLRIMASLVLARKHNTCCNLS
HRFYRLANECAQVLSEVMCMGGSlyVKPGGTSSGDATTAYANSVFNICQAVTANVNALLS
TDGNKIADKYVRNLQHRLYECLYRNRDVEDHEFVDEFYAYLRKHFSMMILSDDAVVCYNNS
YAAQGLVASIKNFKAVALYYQNNVFMSEAKCWTETDLTKGPHEFCSQHTMLVKQGDDYVYL
PYPDPSRILGAGCFVDDIVKTDGTLMIERFVSLAIDAYPLTKHPNQEYADVHLYLYQYIR
KLHDELTHGMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSRLCG
ACIRRPFLCCKCCYDHVISTSHKLVLVSNPYVCNAPGCDVTDVTQLYLGMSYCKSHKP
PISFPLCANGQVFGlyKNTCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLKLFAAET
LKATEETFKLSYGIATVREVLSDRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKVQIGE
YTFEKGDYGDVAVYRGTTTYKLVGDYFVLTSHTVMPLSAPTLPQEHYVRITGLYPTLN
ISDEFSSNVANYQKVGMQKYSTLQGPPTGKSHFAIGLALYYPsARIVYTACSHAADAL
CEKALKYLPIDKCSRIIPARARVECFDKFKVNSTLEQYVFCTVNALPETTADIVVFDEIS
MATNYDLSVVNARLRAKHVYIGDPAQLPAPRTLLTKGTLEPEYFNSVCRLMKTIGPDMF
LGTCCRCPAEIVDTVSAVLDNKLKAHKDKSAQCCKMFYKGVITHDVSSAINRPQIGVVR
EFLTRNPAWRKAVFISPYNsqNAVASKILGLPTQTVDSSQGSEYDYVIFTQTETTETAHSCN
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GLHPTQAPTHLSVDIKFKTEGLCVDIPGIPKDMTYRRLISMGMFKMNYQVNGYPNMFITR
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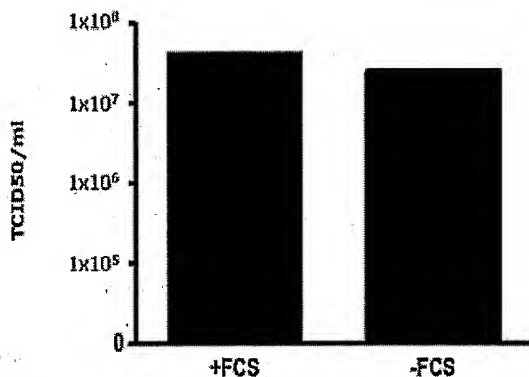
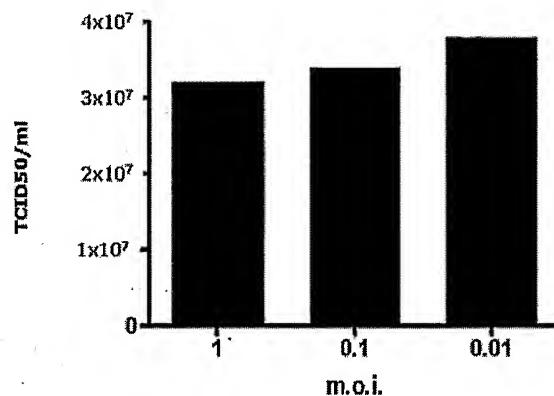
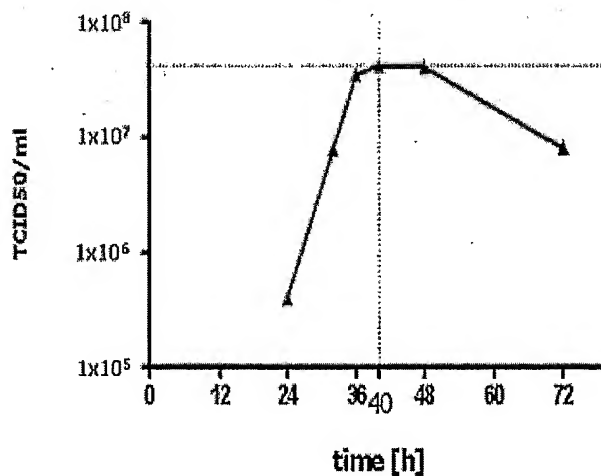
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FIGURE 25

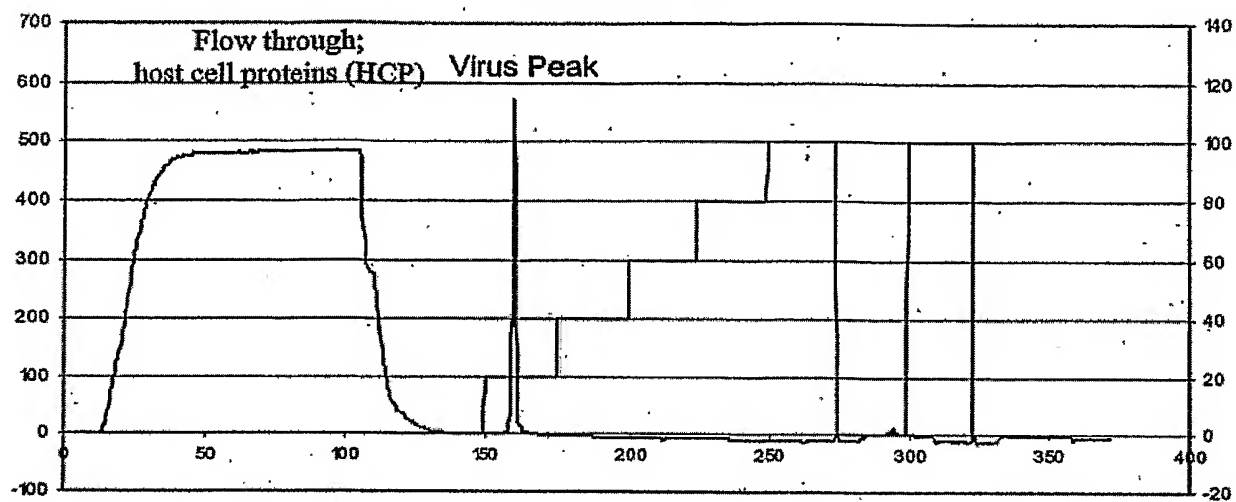
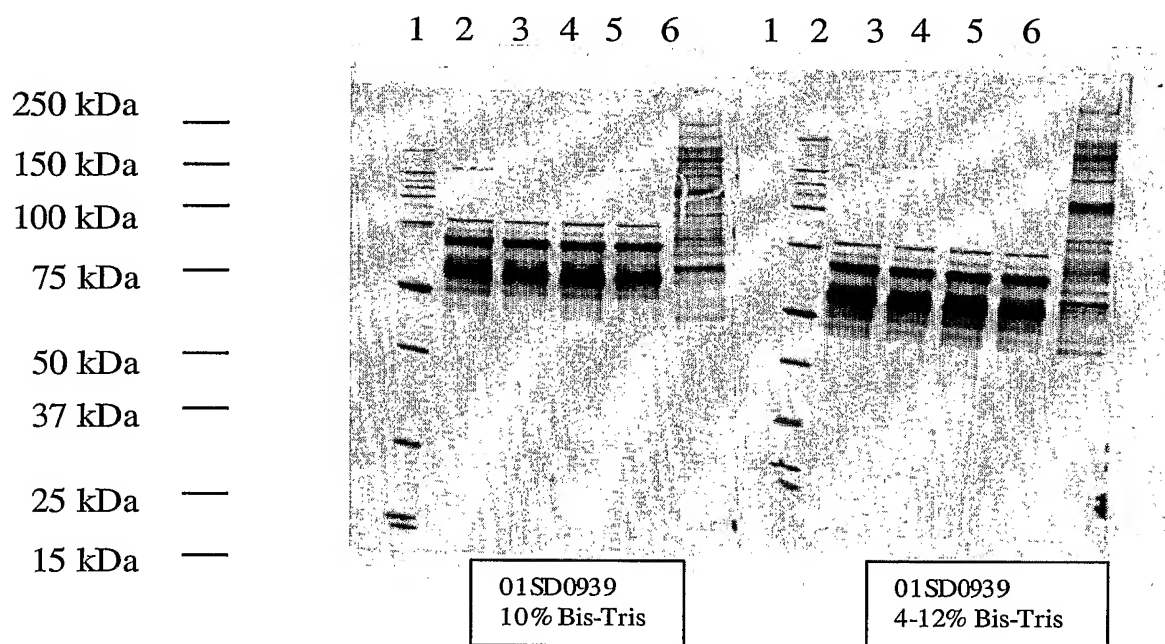
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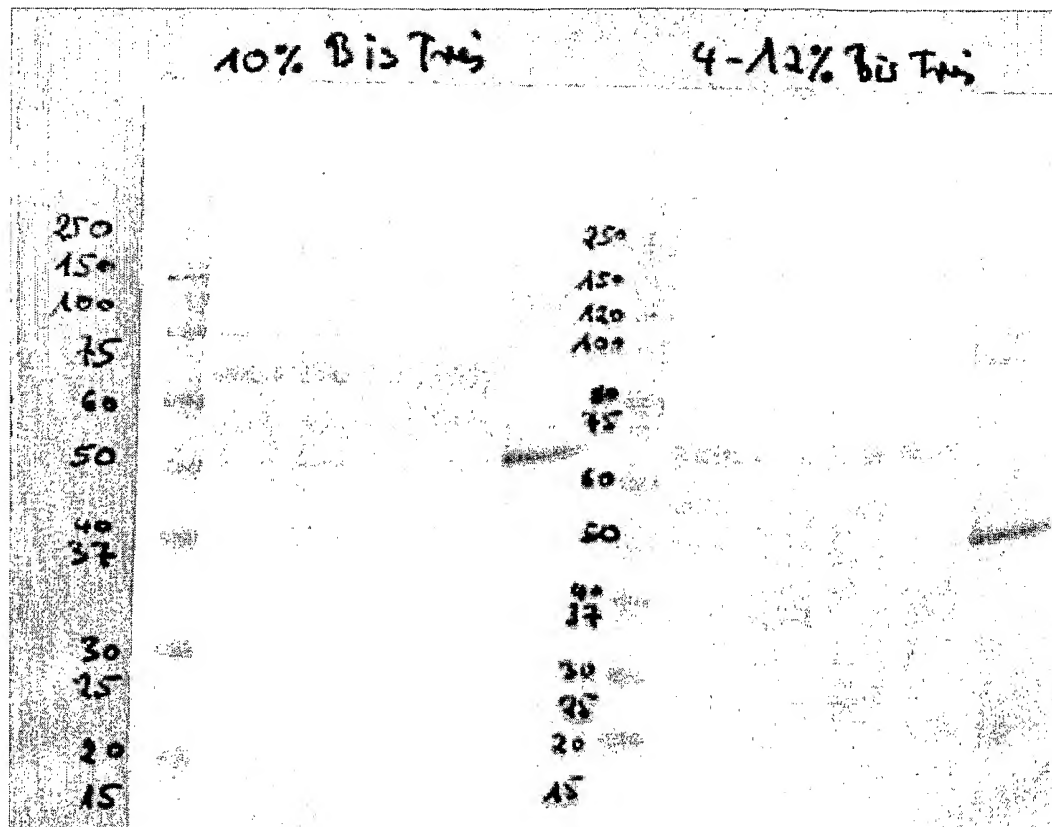
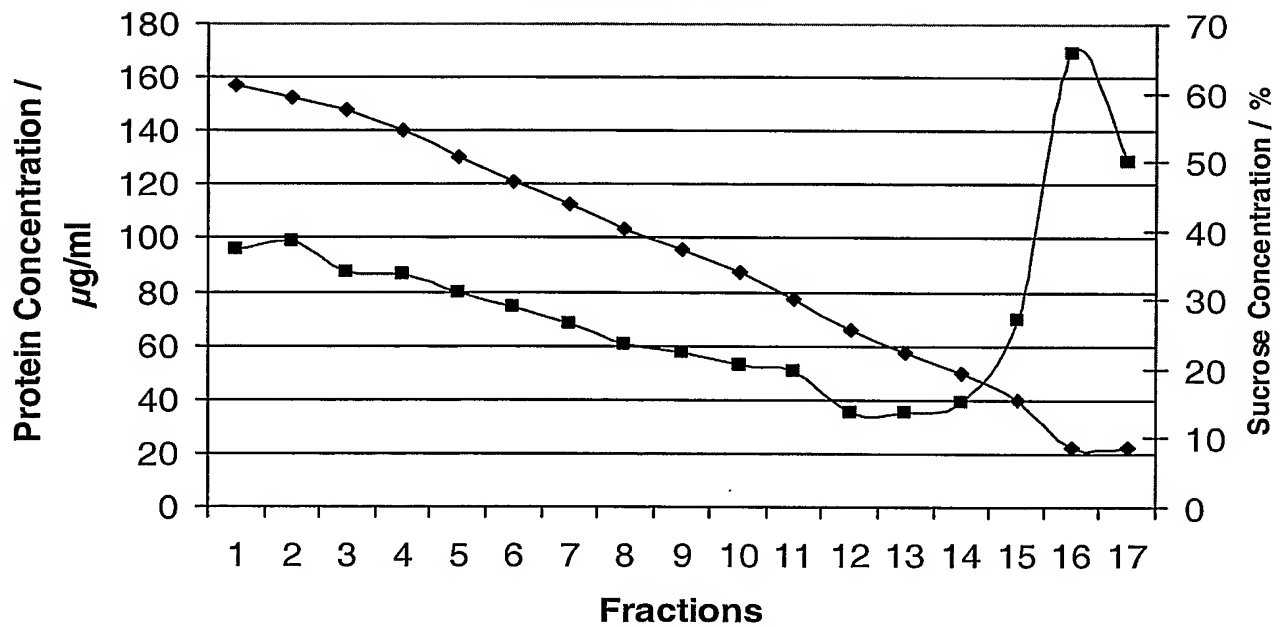
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FIGURE 26**FIGURE 26A****FIGURE 26B****FIGURE 26C**

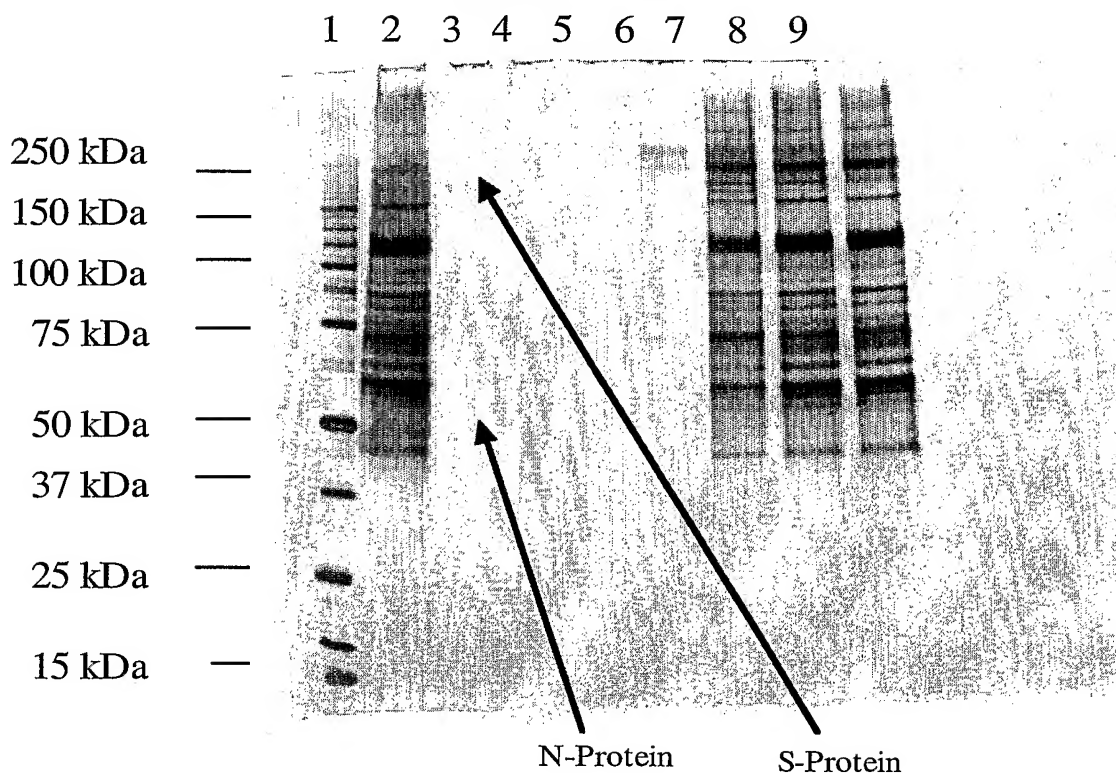
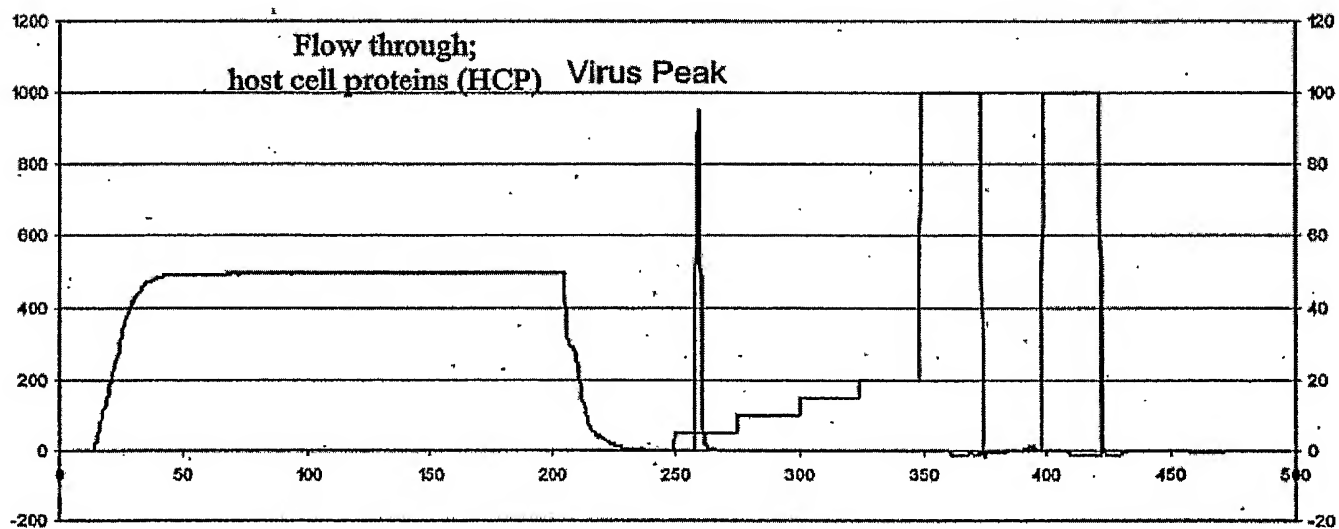
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FIGURE 27**FIGURE 28**

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FIGURE 29**FIGURE 30**

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FIGURE 31**FIGURE 32**

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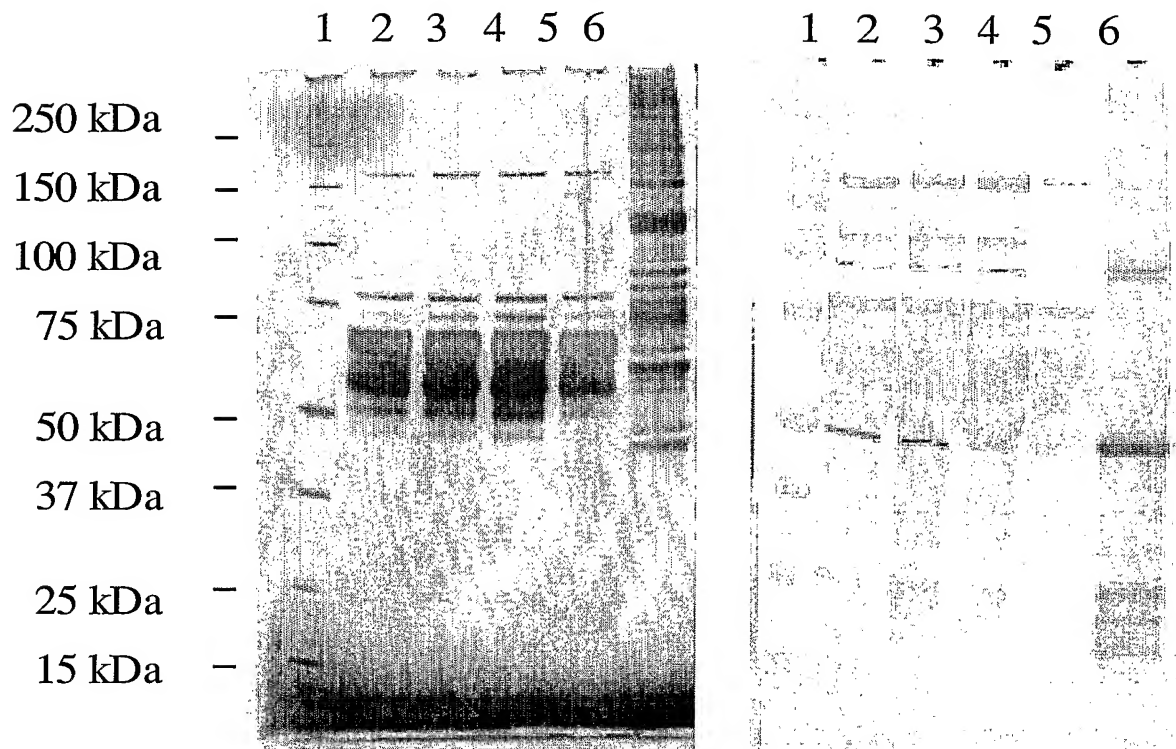
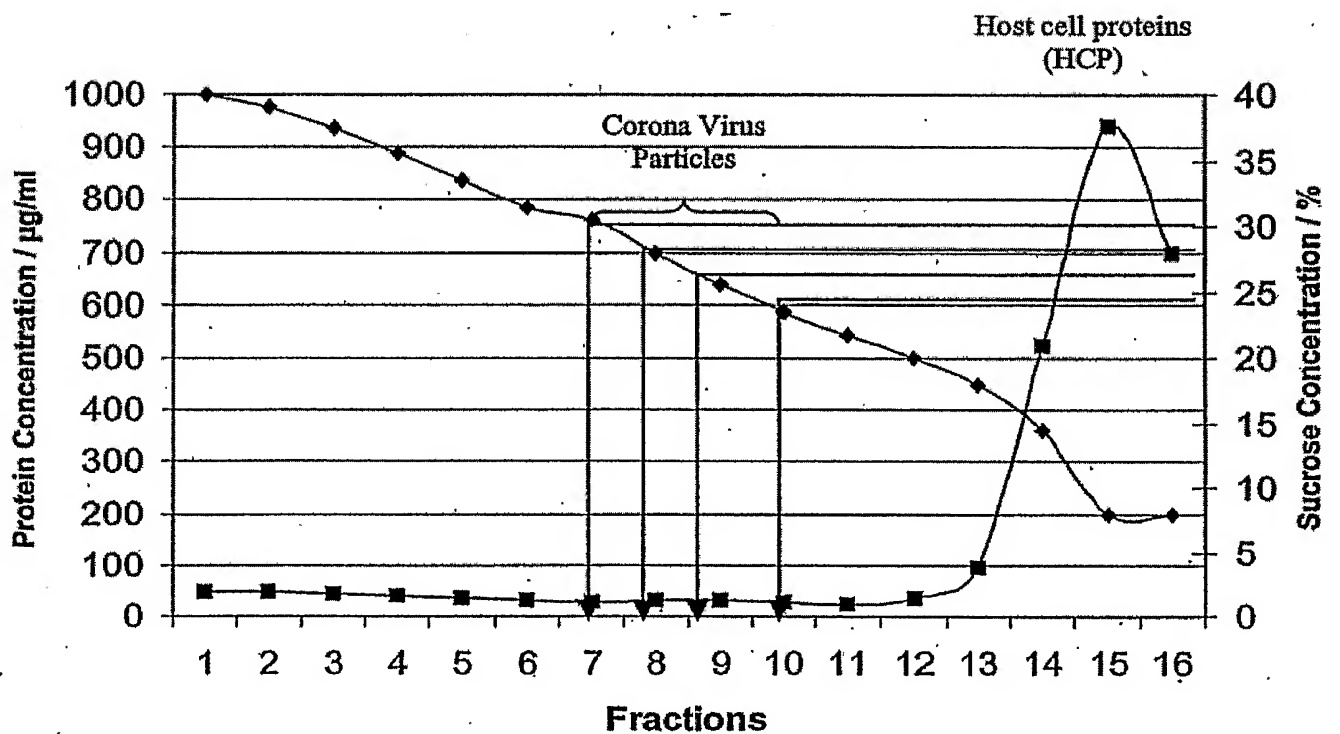
FIGURE 33**FIGURE 34**

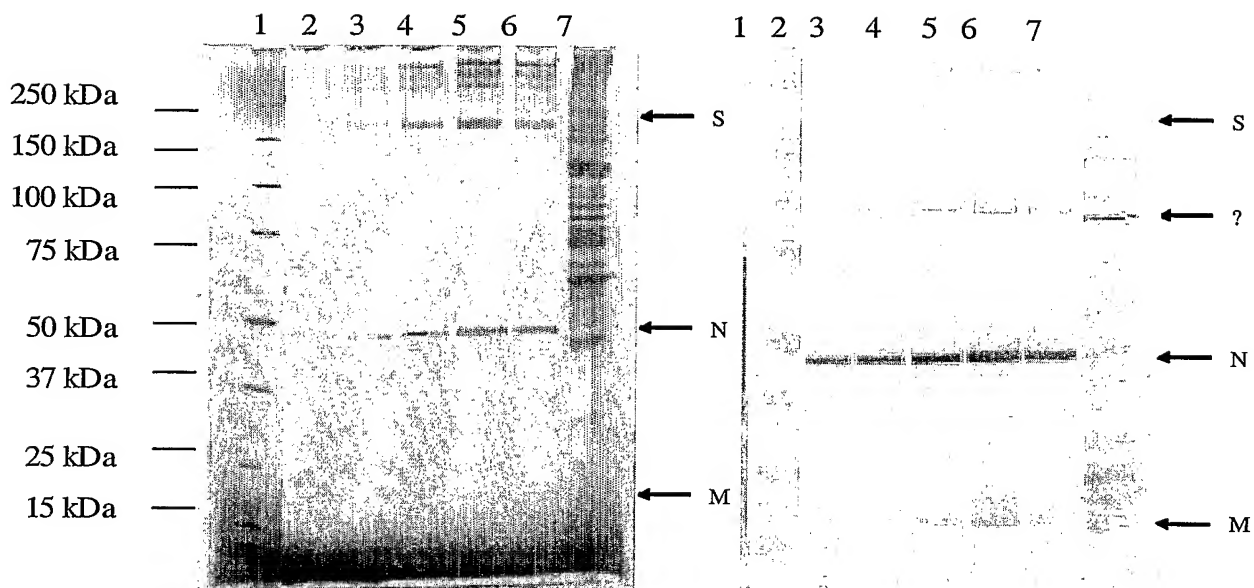
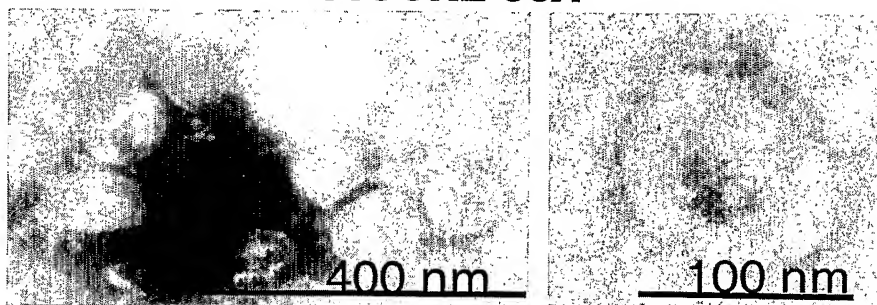
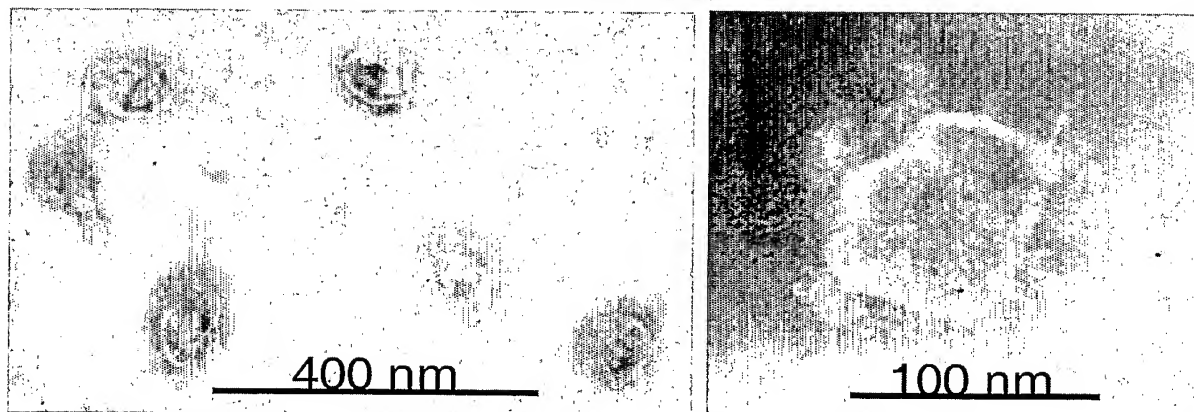
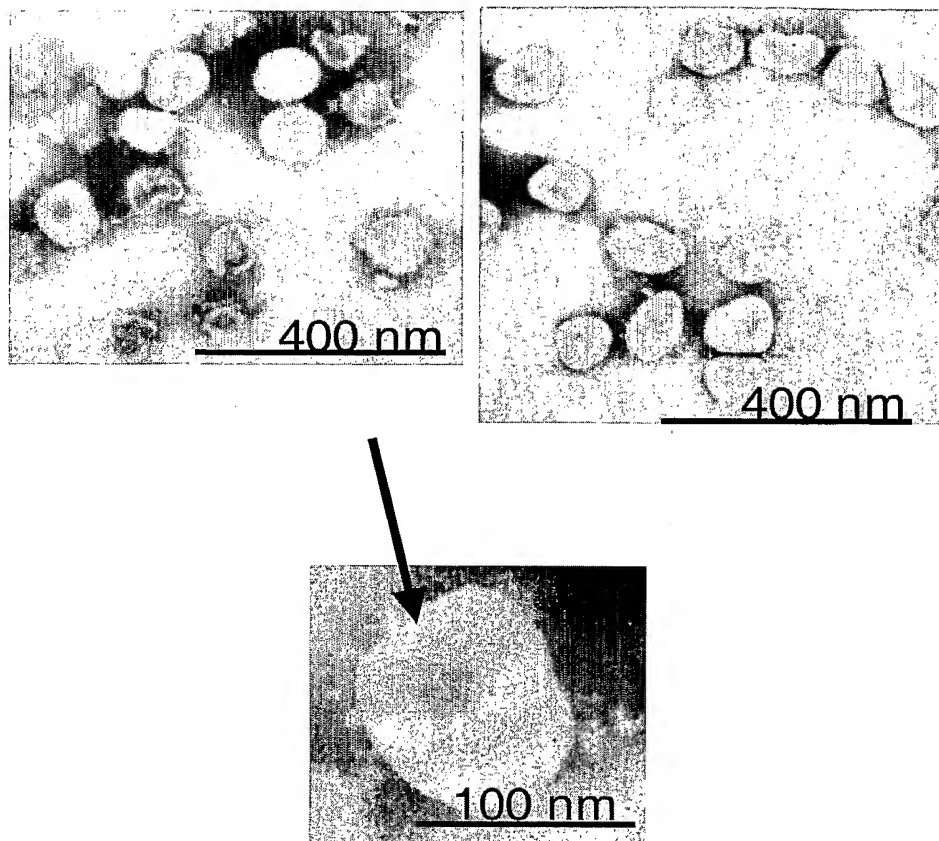
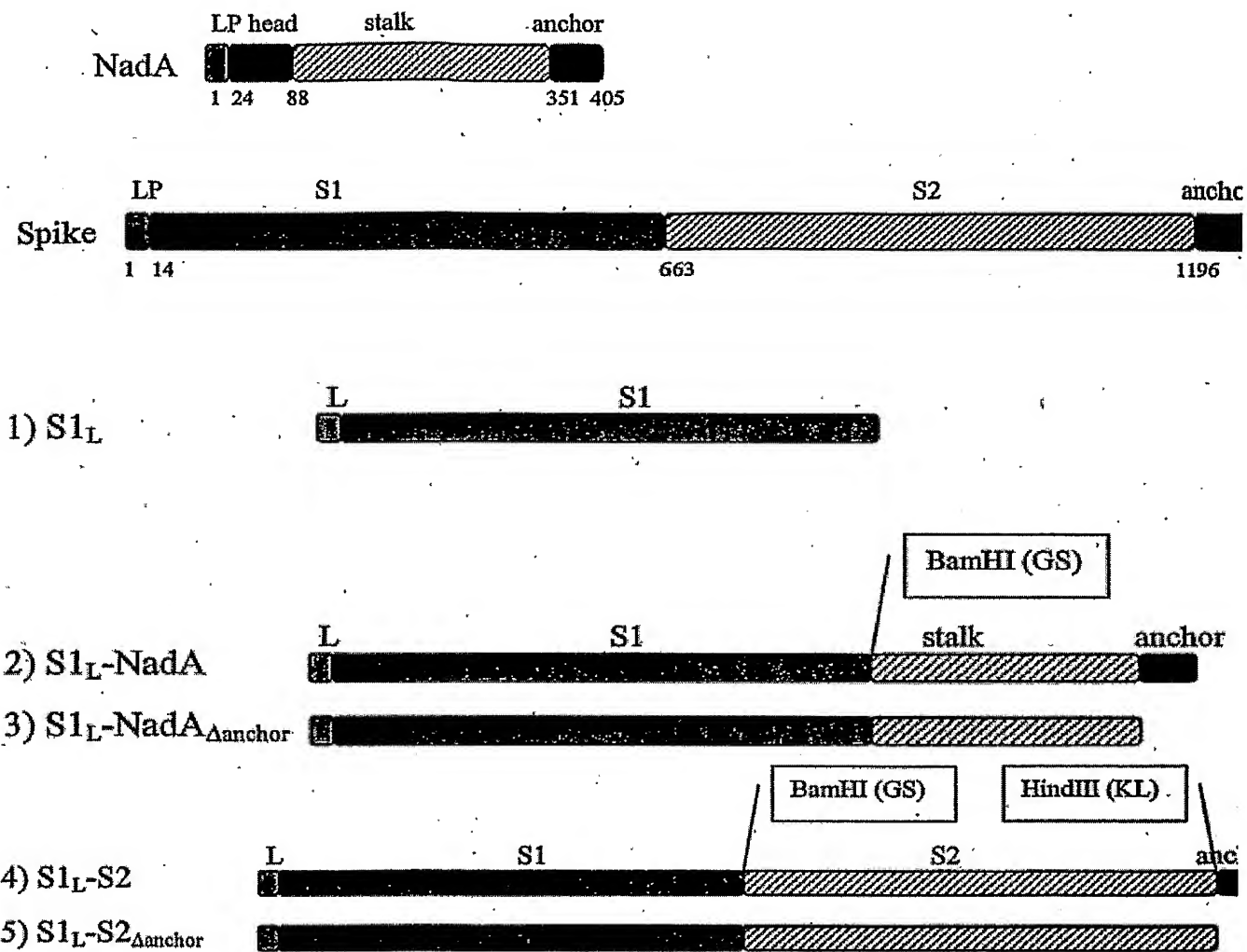
FIGURE 35**FIGURE 36****FIGURE 36A****FIGURE 36B**

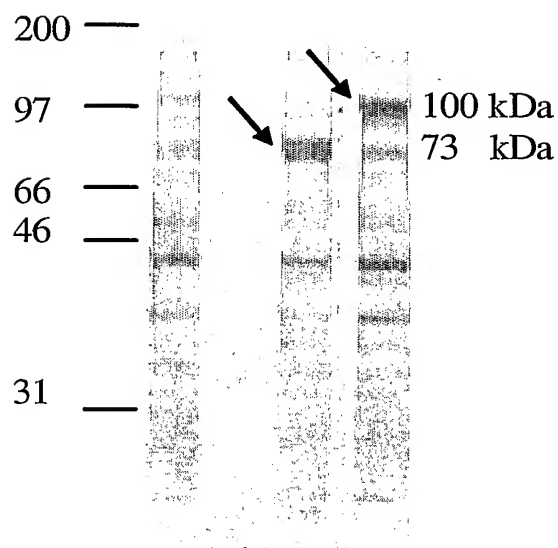
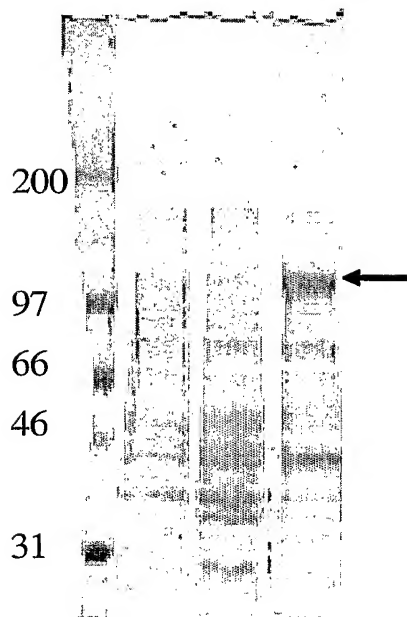
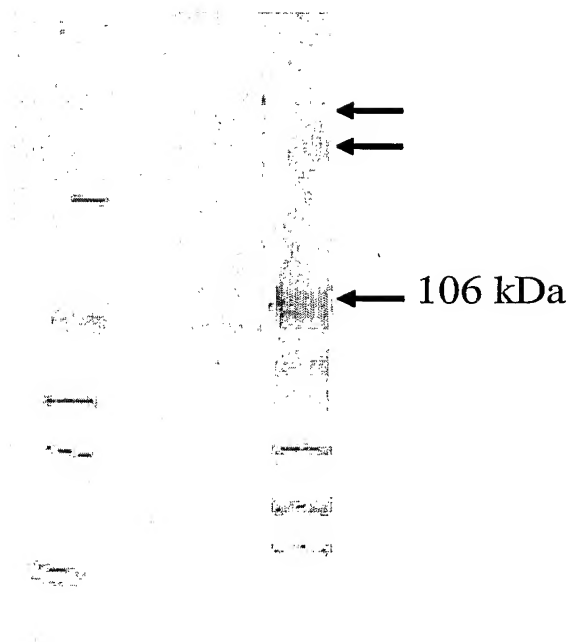
FIGURE 36C



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FIGURE 37

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FIGURE 38**FIGURE 39****FIGURE 39A****FIGURE 39B**

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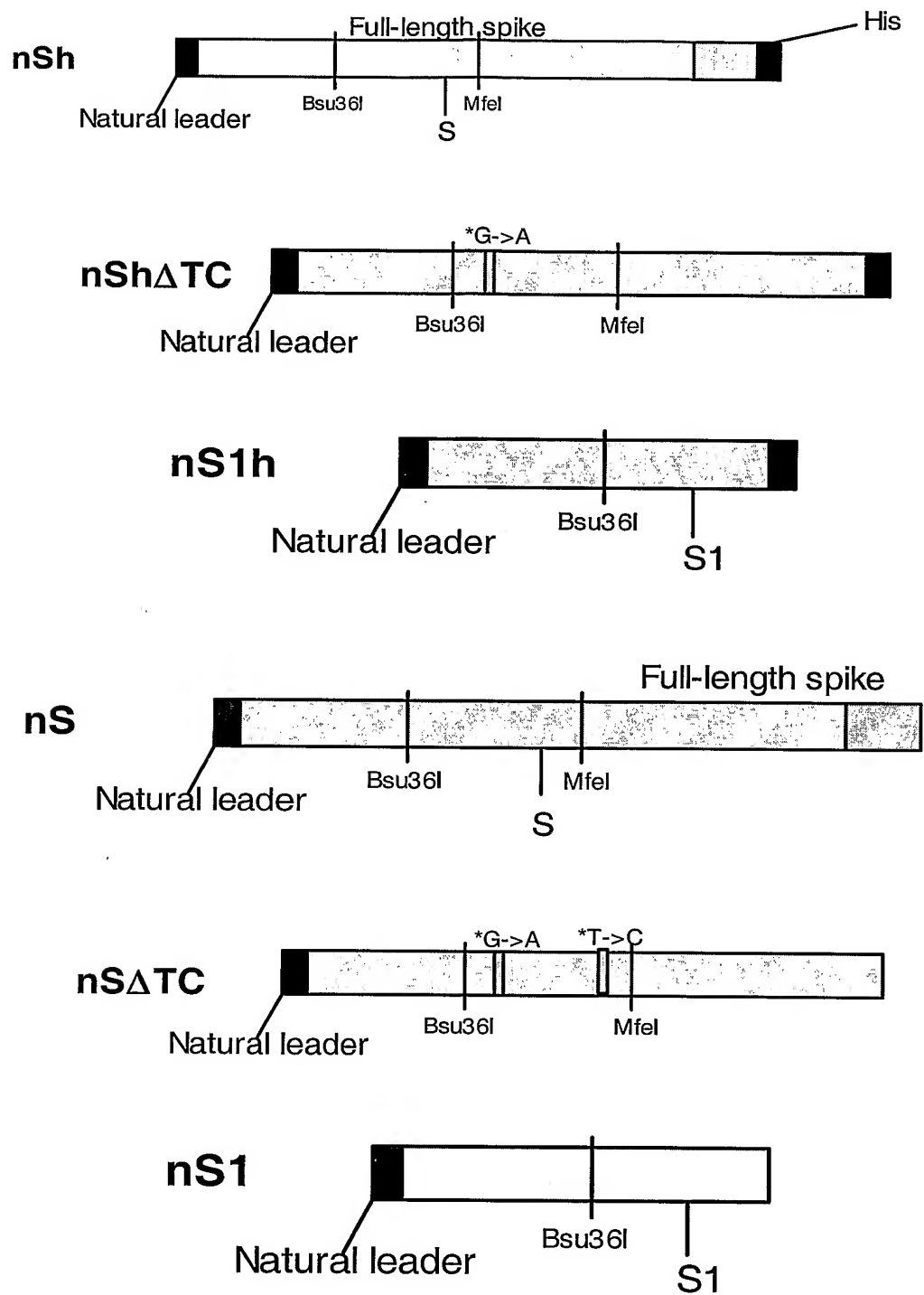
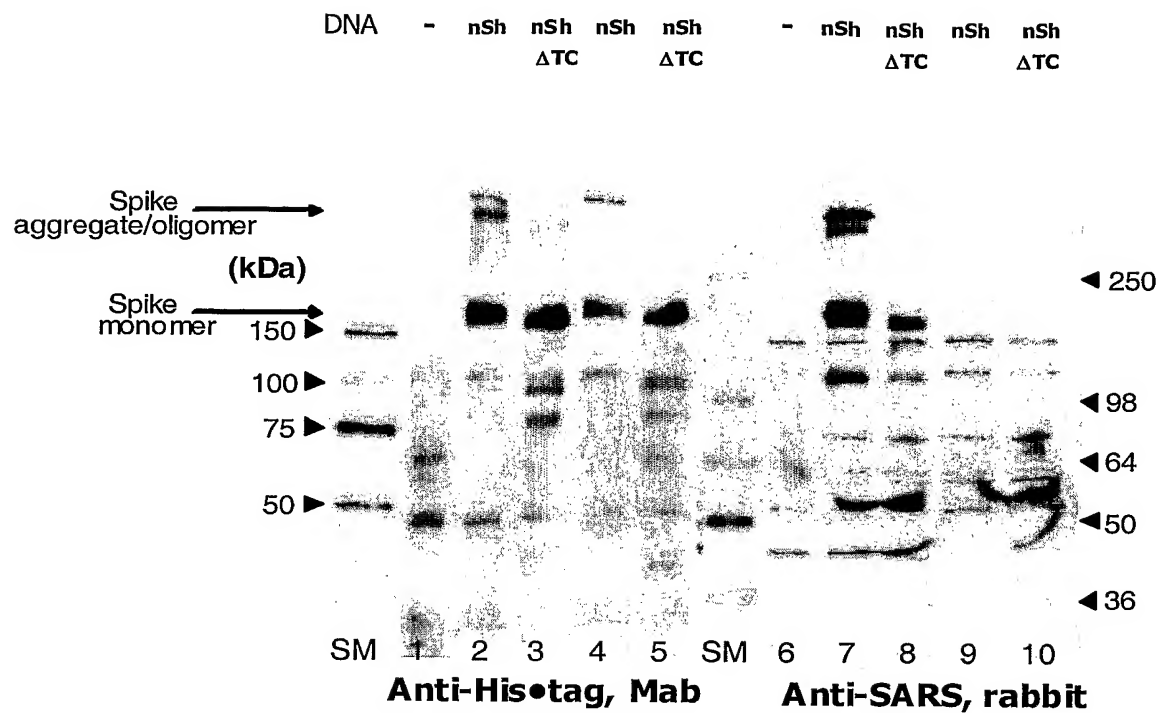
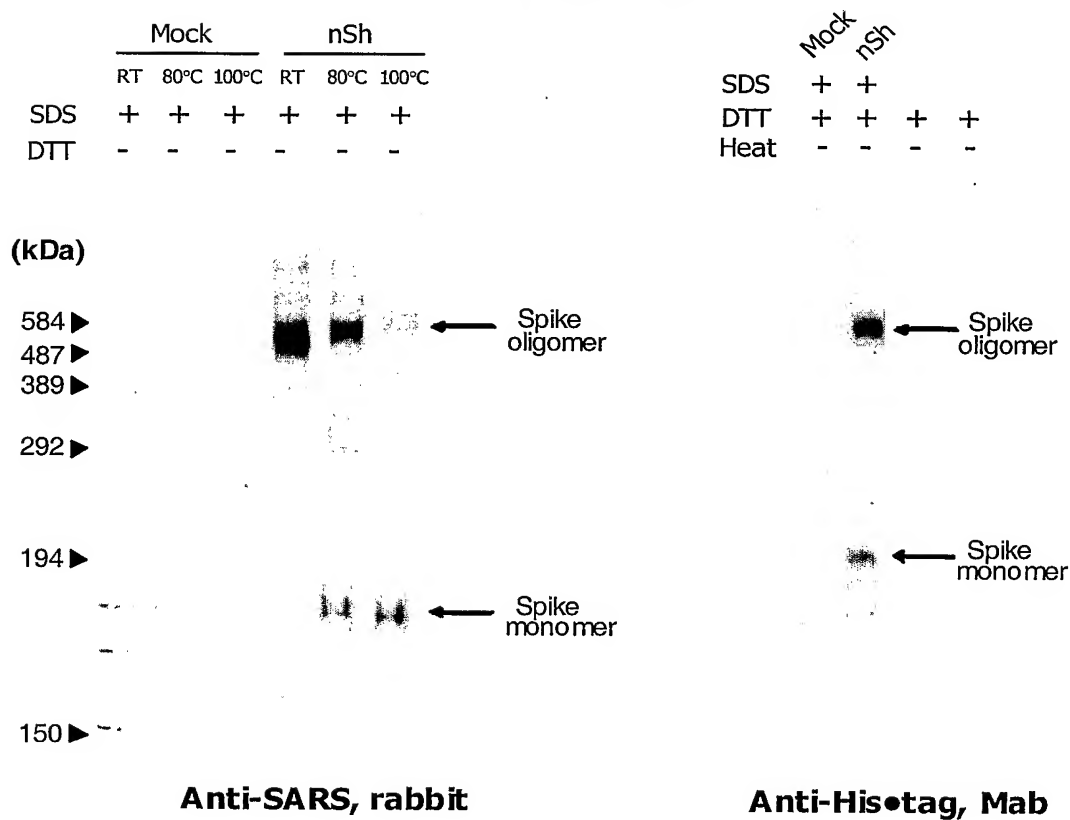
FIGURE 40

FIGURE 41**FIGURE 42**

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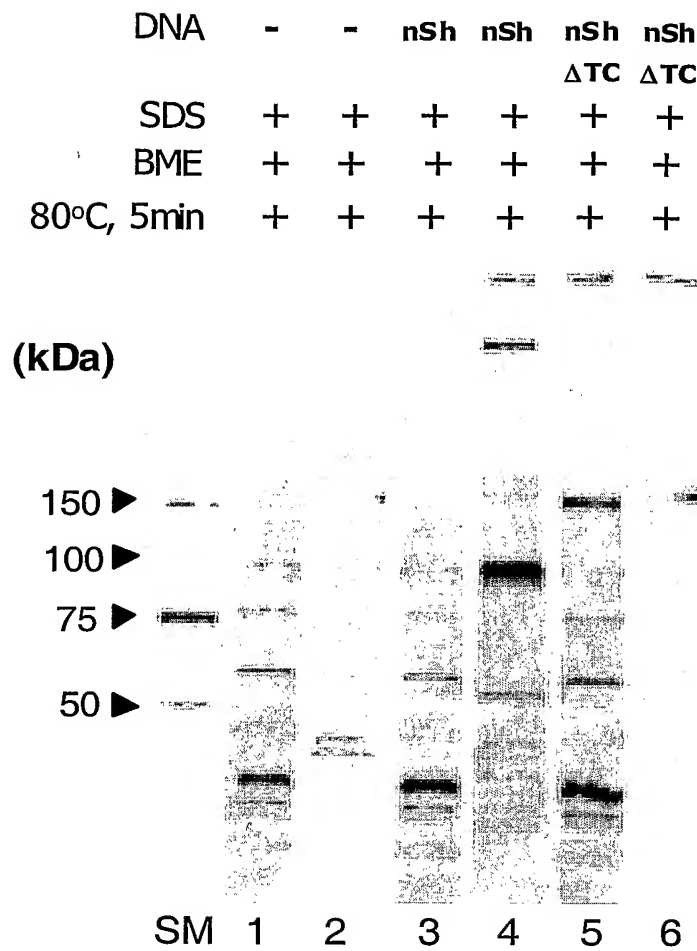
FIGURE 43

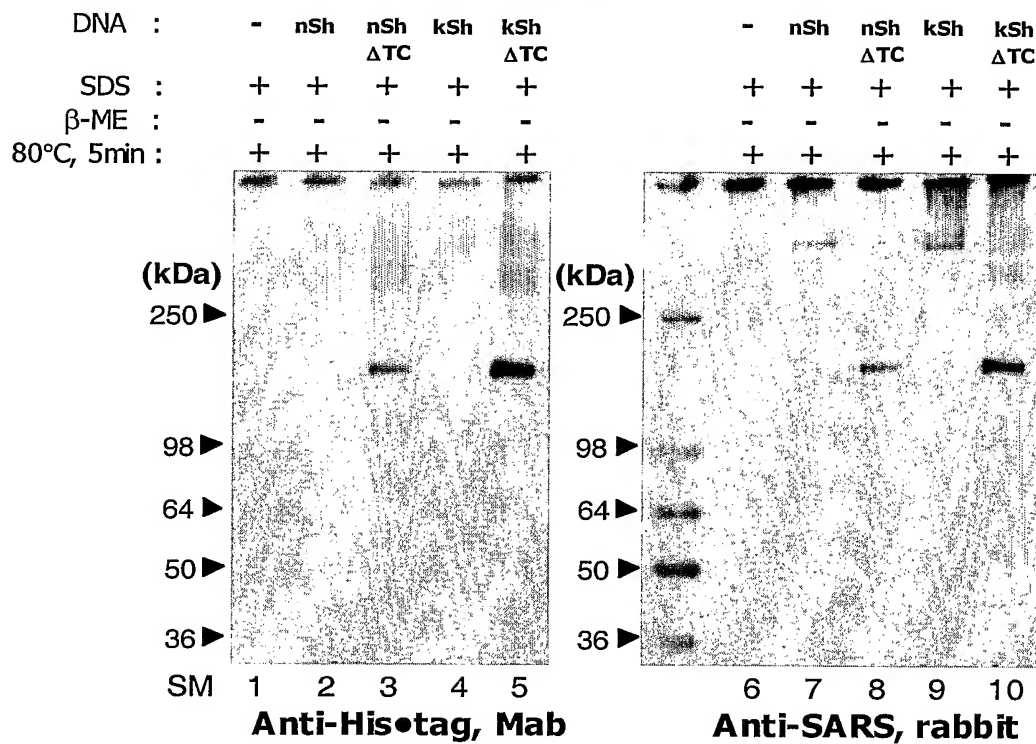
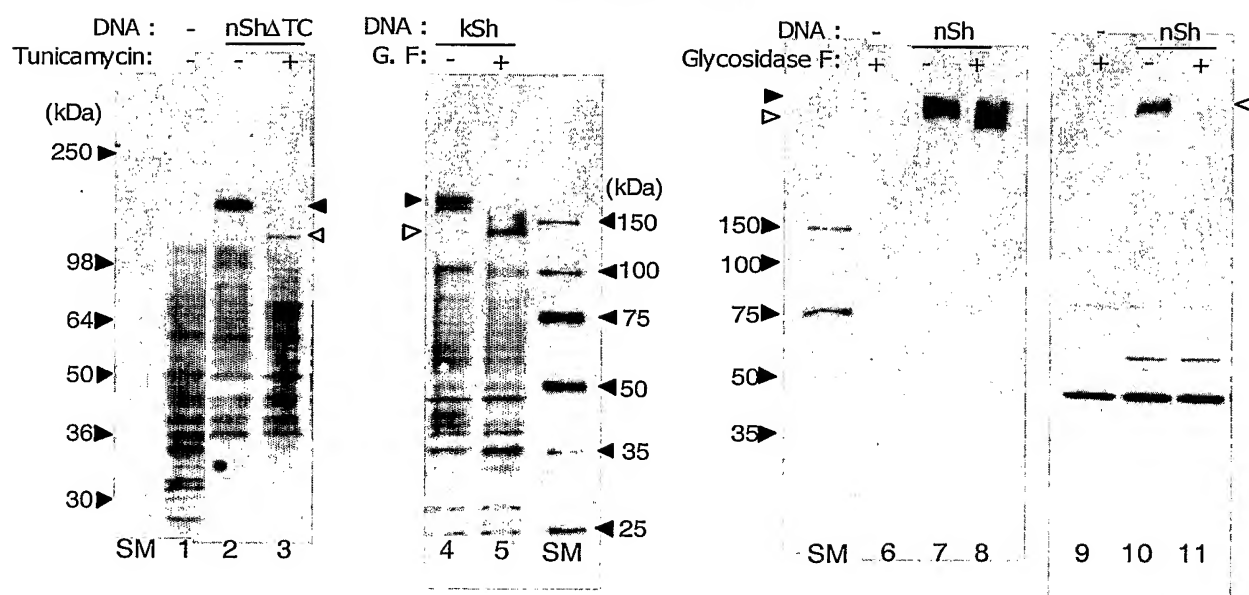
FIGURE 44**FIGURE 45**

FIGURE 46

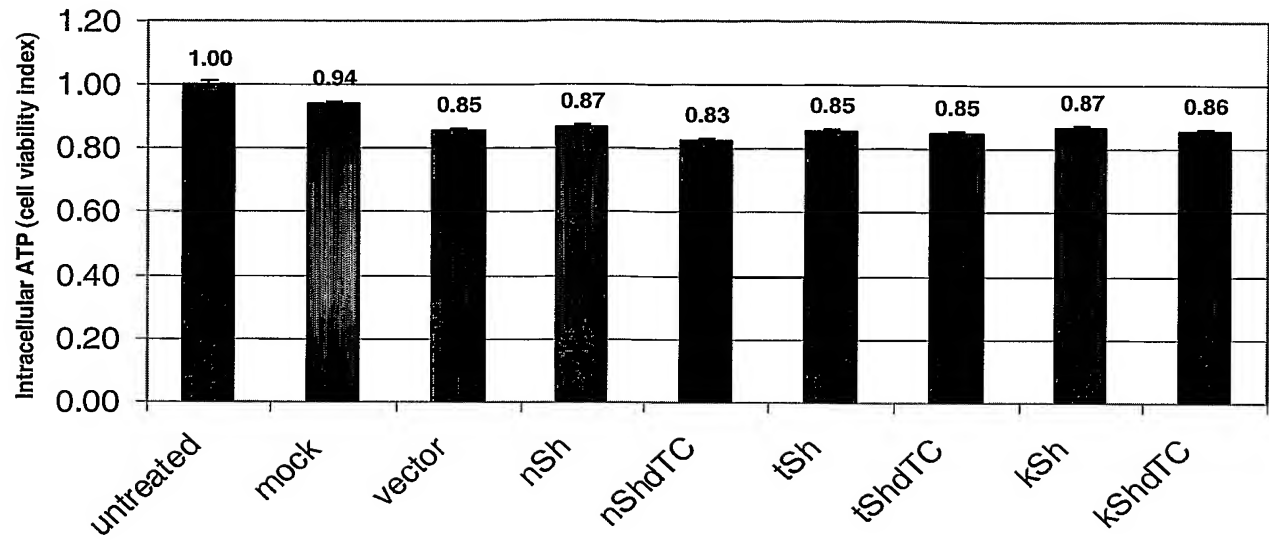
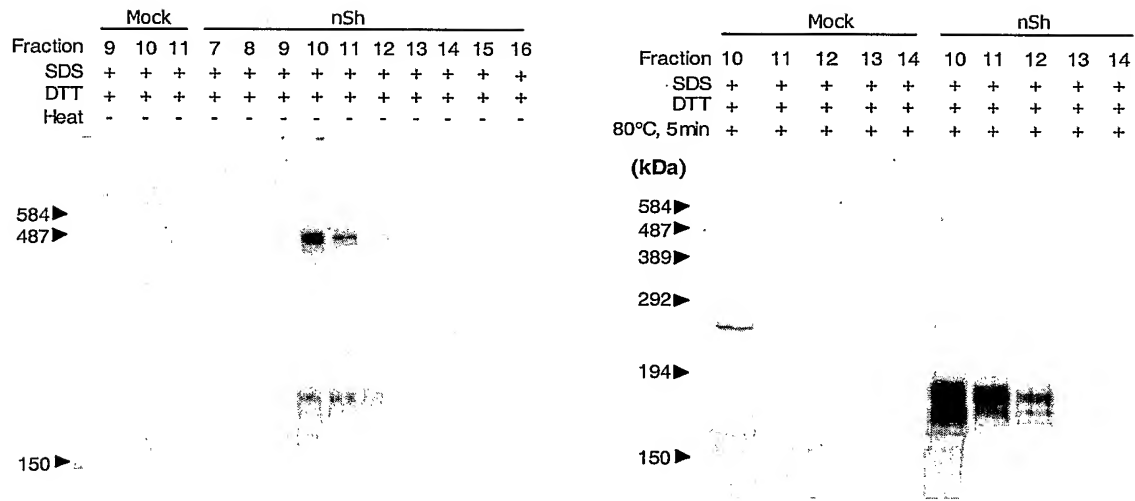
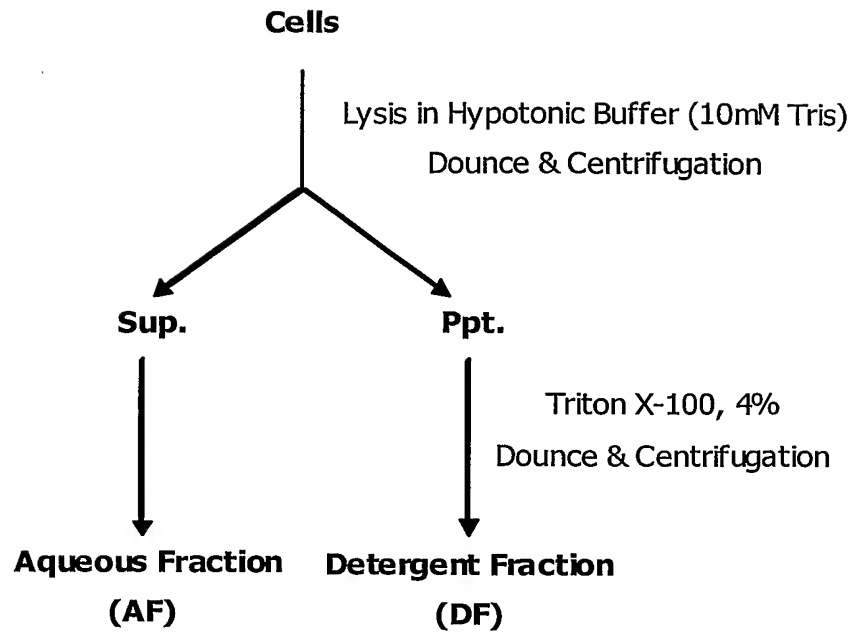
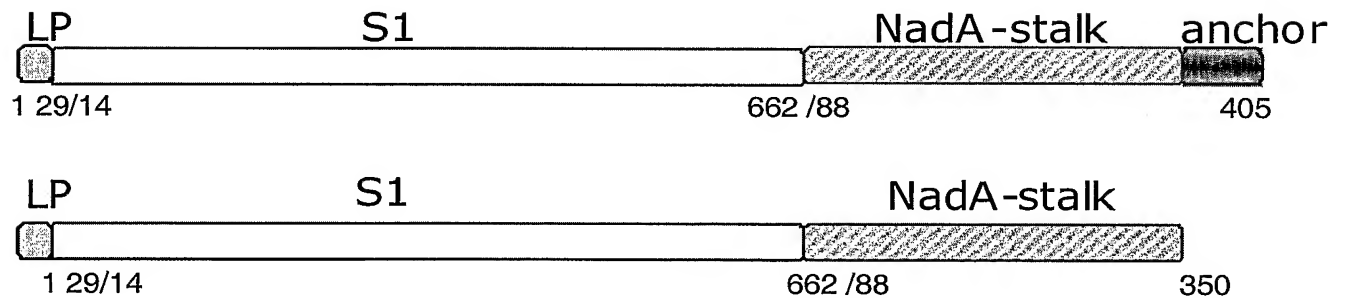


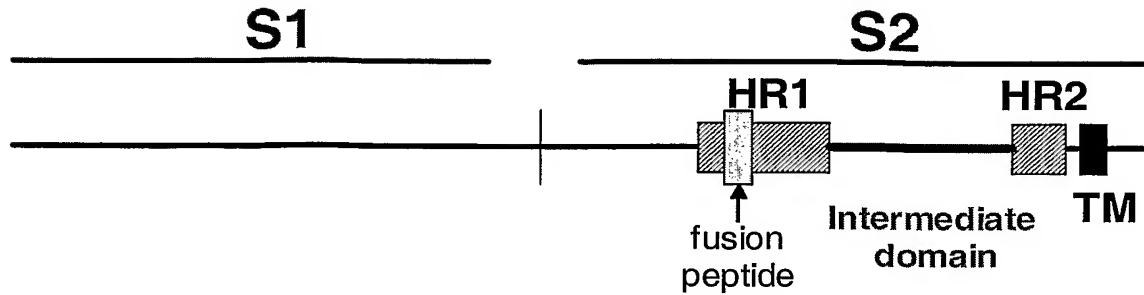
FIGURE 47



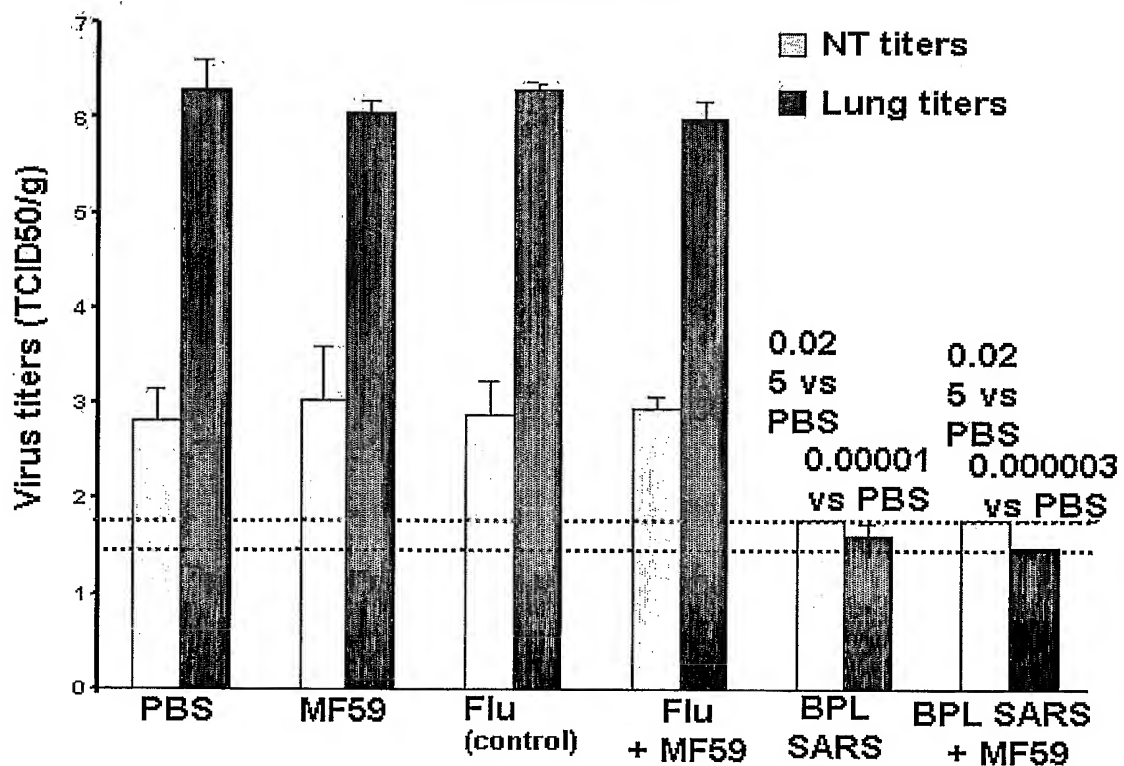
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FIGURE 48**FIGURE 49**

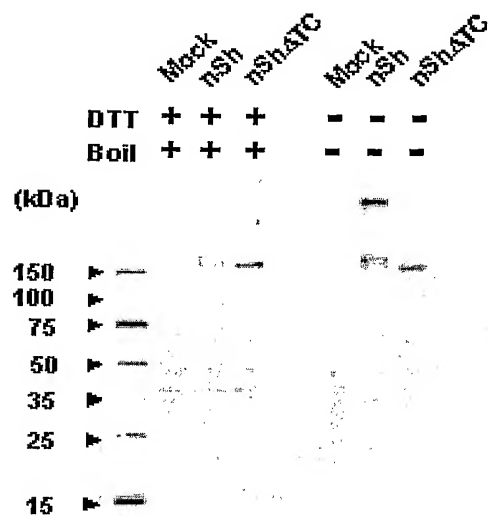
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FIGURE 50

- a) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- b) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)
- c) Leader(NadA)-HR1-intermediate-domain-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- d) Leader(NadA)-HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA)
- e) HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA) - HHHHHH
- f) Leader(NadA)-HR1-intermediate-domain-HR2-anchor(NadA)
- g) Leader(NadA)-HR1-intermediate-domain-HR2

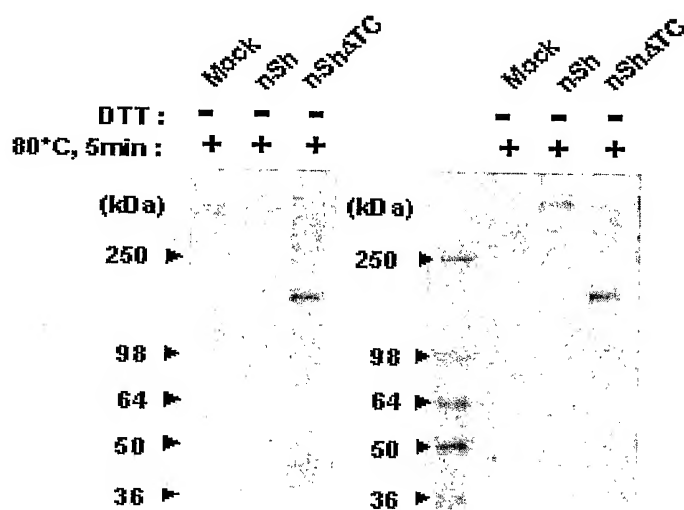
FIGURE 51

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FIGURE 52**A. 293 cell lysates**

Anti-His - tag, mAb

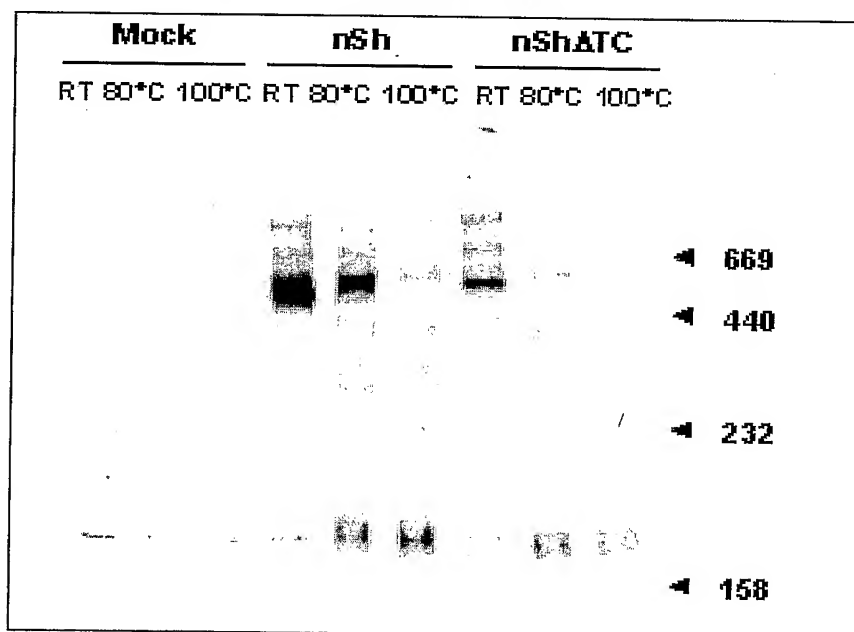
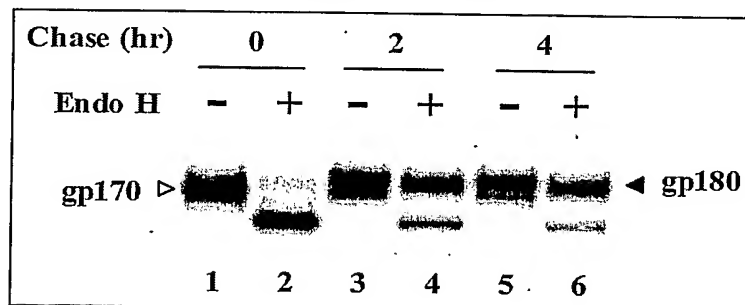
4-20% TG SDS gel

B. COS7 cell culture supernatants

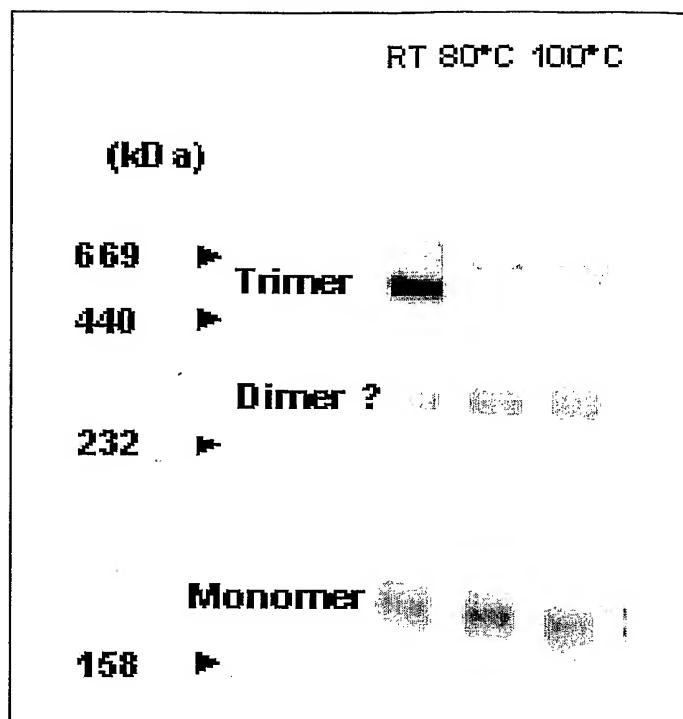
Anti-His - tag, mAb

Anti-SARS, rabbit

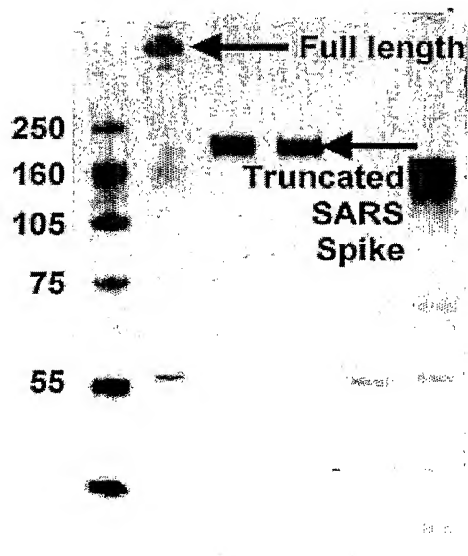
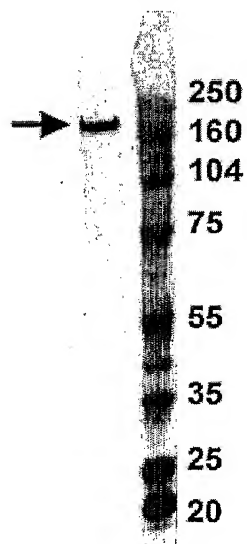
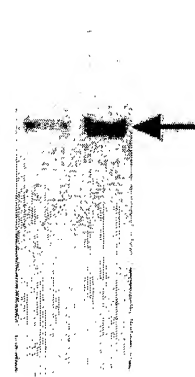
4-20% TG SDS gel

FIGURE 53**FIGURE 55**

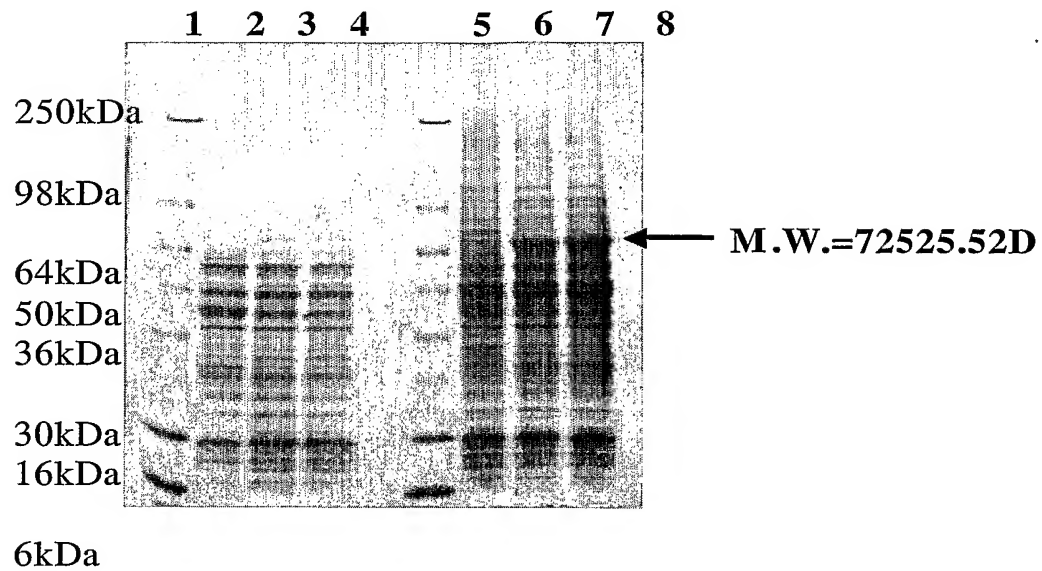
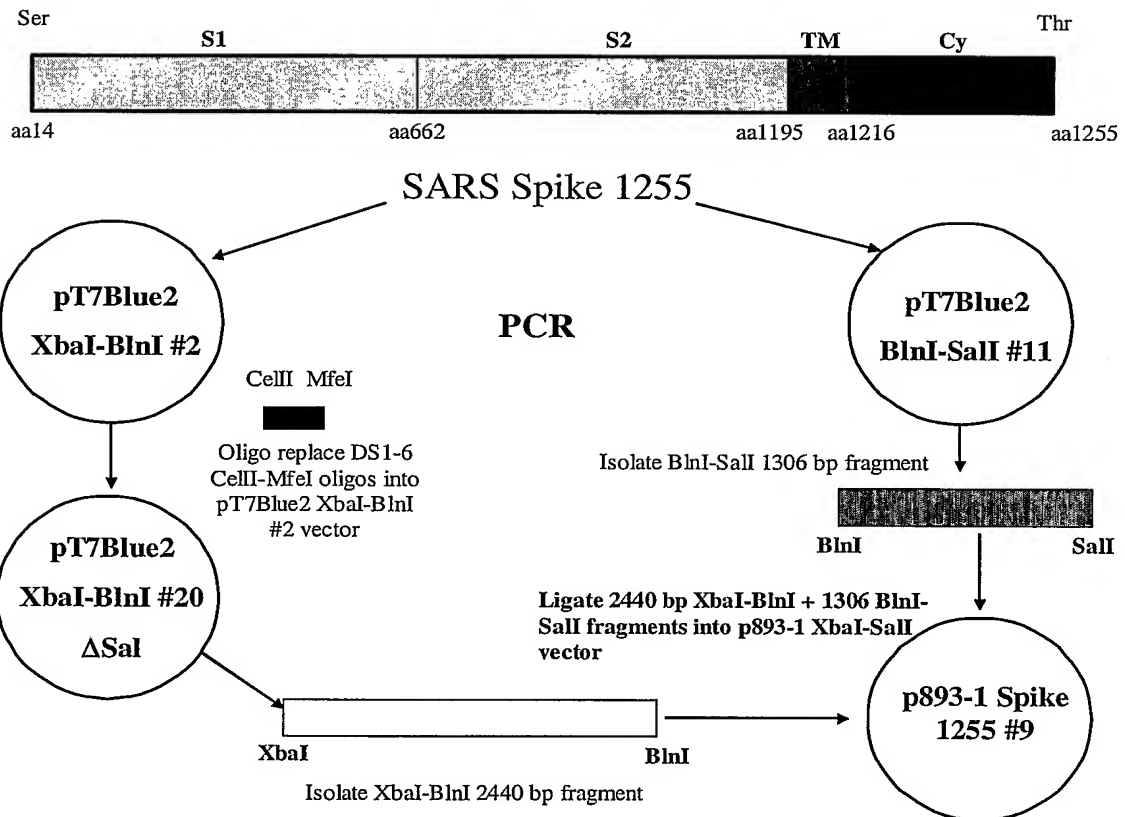
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FIGURE 54**FIGURE 56****FIGURE 56A**

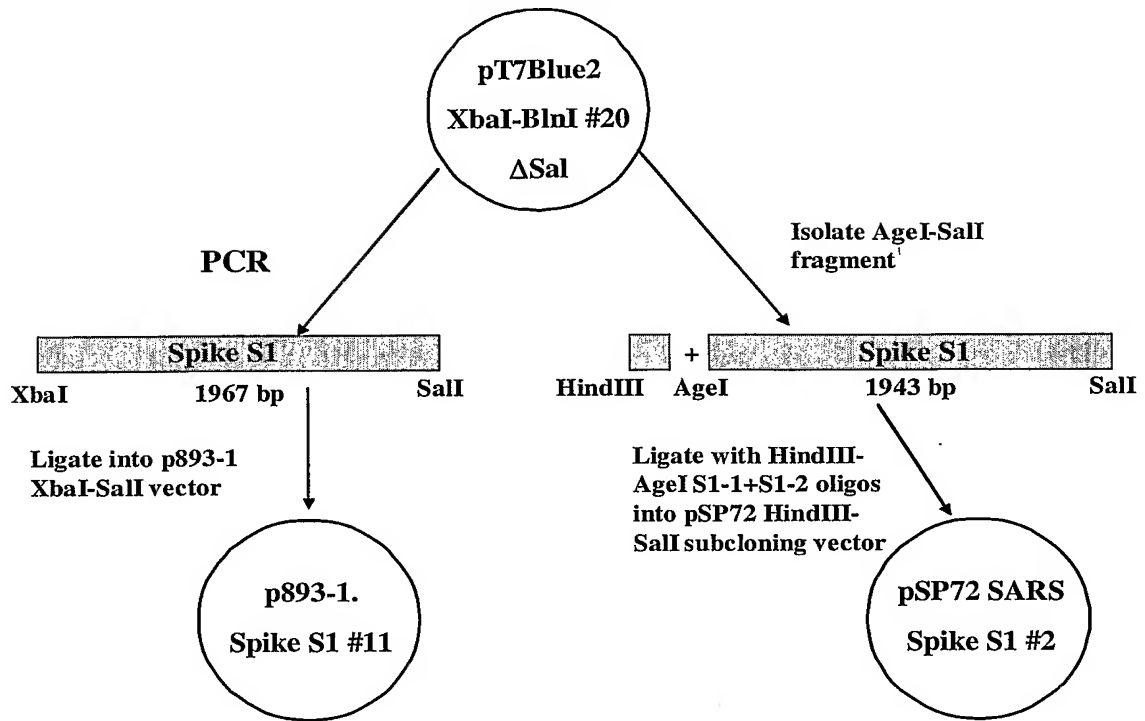
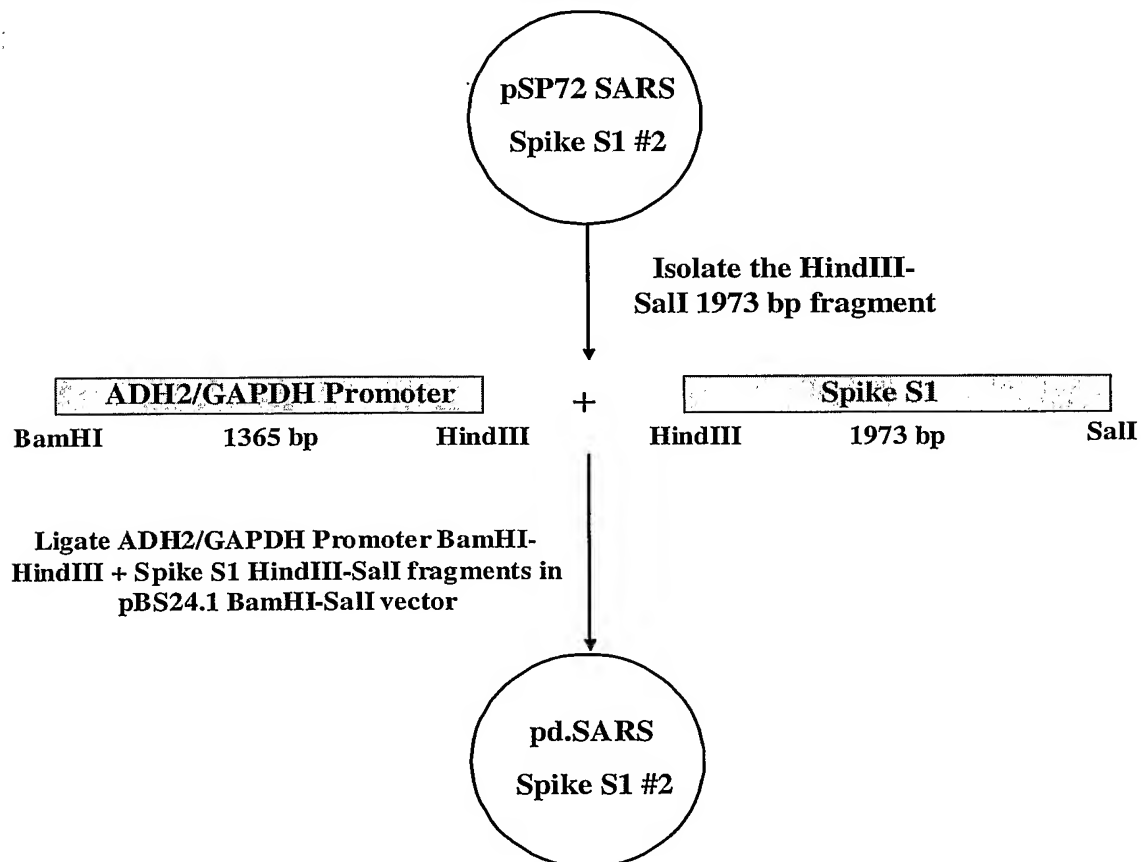
Hours: 48 72

**FIGURE 56B****FIGURE 56C**

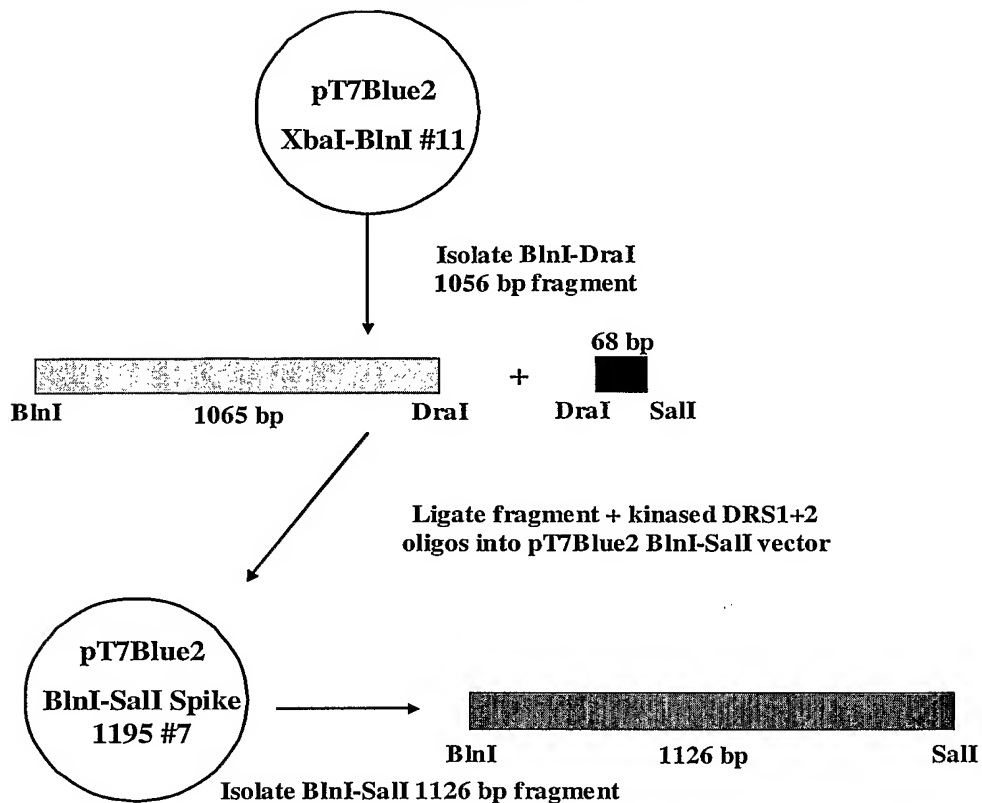
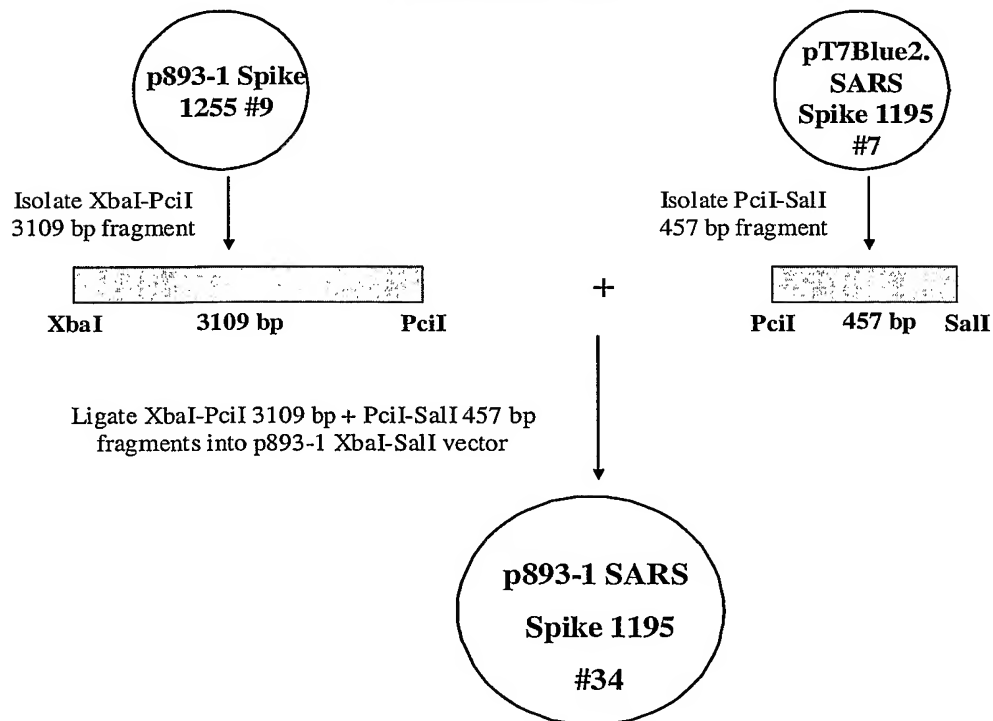
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FIGURE 57**FIGURE 58**

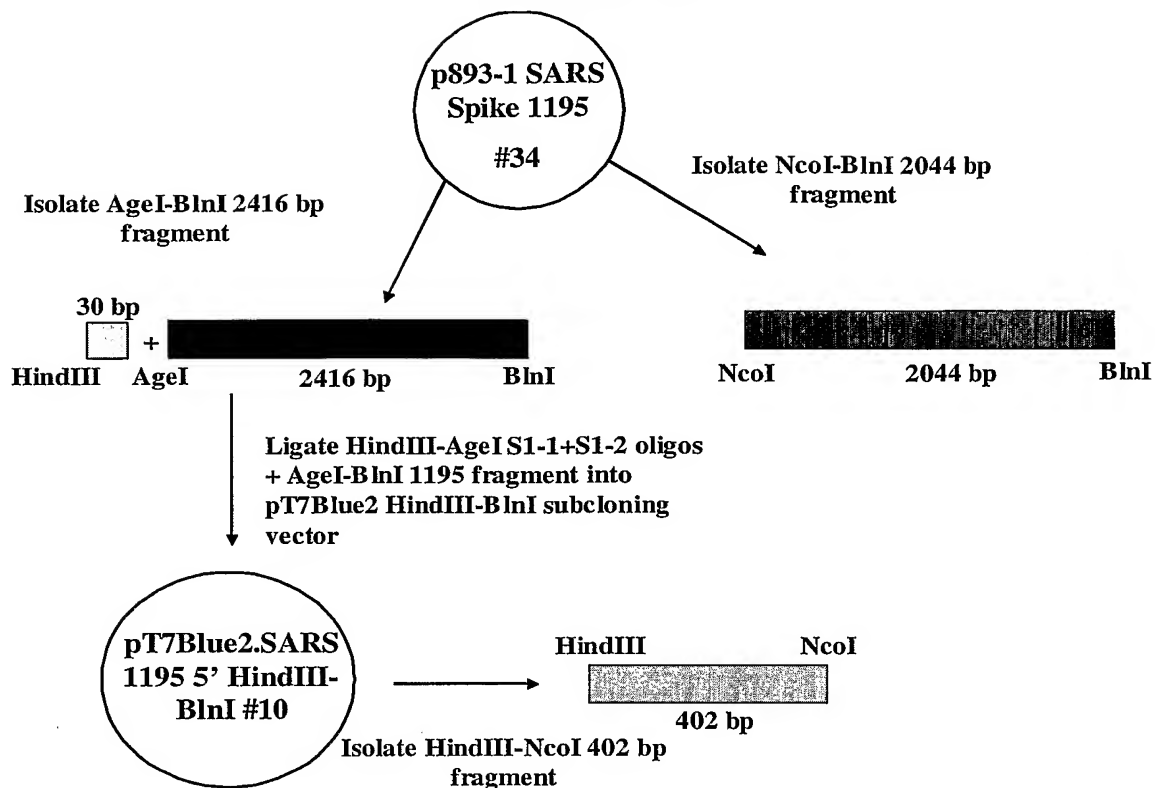
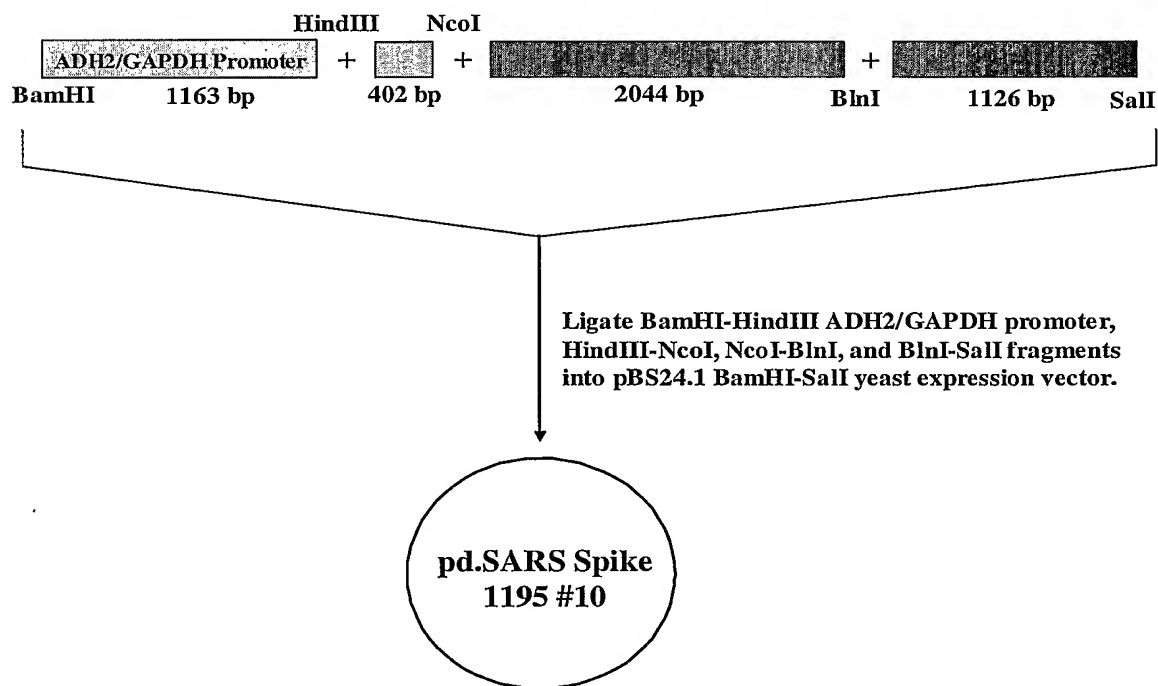
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FIGURE 59**FIGURE 60**

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FIGURE 61**FIGURE 62**

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FIGURE 63**FIGURE 64**

| | | | | | | | | | | | | | | | |
|------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | | | 1 | | | | | | | | | | 10 |
| AAGCTTACAAAACAAA | | | | | M | S | D | L | D | R | C | T | T | F | |
| | | | | | ATG | AGT | GAC | CTT | GAC | CGG | TGC | ACC | ACT | TTT | |
| | | | | | 20 | | | | | | | | | | |
| D | D | V | Q | A | P | N | Y | T | Q | H | T | S | S | M | |
| GAT | GAT | GTT | CAA | GCT | CCT | AAT | TAC | ACT | CAA | CAT | ACT | TCA | TCT | ATG | |
| | | | | | 30 | | | | | | | | | | 40 |
| R | G | V | Y | Y | P | D | E | I | F | R | S | D | T | L | |
| AGG | GGG | GTT | TAC | TAT | CCT | GAT | GAA | ATT | TTT | AGA | TCA | GAC | ACT | CTT | |
| | | | | | 50 | | | | | | | | | | |
| Y | L | T | Q | D | L | F | L | P | F | Y | S | N | V | T | |
| TAT | TTA | ACT | CAG | GAT | TTA | TTT | CTT | CCA | TTT | TAT | TCT | AAT | GTT | ACA | |
| | | | | | 60 | | | | | | | | | | 70 |
| G | F | H | T | I | N | H | T | F | G | N | P | V | I | P | |
| GGG | TTT | CAT | ACT | ATT | AAT | CAT | ACG | TTT | GGC | AAC | CCT | GTC | ATA | CCT | |
| | | | | | 80 | | | | | | | | | | |
| F | K | D | G | I | Y | F | A | A | T | E | K | S | N | V | |
| TTT | AAG | GAT | GGT | ATT | TAT | TTT | GCT | GCC | ACA | GAG | AAA | TCA | AAT | GTT | |
| | | | | | 90 | | | | | | | | | | 100 |
| V | R | G | W | V | F | G | S | T | M | N | N | K | S | Q | |
| GTC | CGT | GGT | TGG | GTT | TTT | GGT | TCT | ACC | ATG | AAC | AAC | AAG | TCA | CAG | |
| | | | | | 110 | | | | | | | | | | |
| S | V | I | I | I | N | N | S | T | N | V | V | I | R | A | |
| TCG | GTG | ATT | ATT | ATT | AAC | AAT | TCT | ACT | AAT | GTT | GTT | ATA | CGA | GCA | |
| | | | | | 120 | | | | | | | | | | 130 |
| C | N | F | E | L | C | D | N | P | F | F | A | V | S | K | |
| TGT | AAC | TTT | GAA | TTG | TGT | GAC | AAC | CCT | TTC | TTT | GCT | GTT | TCT | AAA | |
| | | | | | 140 | | | | | | | | | | |
| P | M | G | T | Q | T | H | T | M | I | F | D | N | A | F | |
| CCC | ATG | GGT | ACA | CAG | ACA | CAT | ACT | ATG | ATA | TTC | GAT | AAT | GCA | TTT | |
| | | | | | 150 | | | | | | | | | | 160 |
| N | C | T | F | E | Y | I | S | D | A | F | S | L | D | V | |
| AAT | TGC | ACT | TTC | GAG | TAC | ATA | TCT | GAT | GCC | TTT | TCG | CTT | GAT | GTT | |
| | | | | | 170 | | | | | | | | | | |
| S | E | K | S | G | N | F | K | H | L | R | E | F | V | F | |
| TCA | GAA | AAG | TCA | GGT | AAT | TTT | AAA | CAC | TTA | CGA | GAG | TTT | GTG | TTT | |
| | | | | | 180 | | | | | | | | | | 190 |
| K | N | K | D | G | F | L | Y | V | Y | K | G | Y | Q | P | |
| AAA | AAT | AAA | GAT | GGG | TTT | CTC | TAT | GTT | TAT | AAG | GGC | TAT | CAA | CCT | |

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200
I D V V R D L P S G F N T L K
ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA

210
P I F K L P L G I N I T N F R
CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA

220
A I L T A F S P A Q D I W G T
GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG

230
S A A A Y F V G Y L K P T T F
TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT

240
M L K Y D E N G T I T D A V D
ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT

250
C S Q N P L A E L K C S V K S
TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC

260
F E I D K G I Y Q T S N F R V
TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT

270
V P S G D V V R F P N I T N L
GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG

280
C P F G E V F N A T K F P S V
TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC

290
Y A W E R K K I S N C V A D Y
TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC

300
S V L Y N S T F F S T F K C Y
TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT

310
G V S A T K L N D L C F S N V
GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC

320
Y A D S F V V K G D D V R Q I
TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA

330
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

340
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

350
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

360
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

370
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

380
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

390
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

400
A P G Q T G V I A D Y N Y K L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

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410
 P D D F M G C V L A W N T R N
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC

420
 I D A T S T G N Y N Y K Y R Y
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT

440
 L R H G K L R P F E R D I S N
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT

450
 V P F S P D G K P C T P P A L
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT

470
 N C Y W P L N D Y G F Y T T T
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT

480
 G I G Y Q P Y R V V V L S F E
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA

500
 L L N A P A T V C G P K L S T
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT

510
 D L I K N Q C V N F N F N G L
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC

530
 T G T G V L T P S S K R F Q P
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA

540
 F Q Q F G R D V S D F T D S V
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT

560
 R D P K T S E I L D I S P C S
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT

570
 F G G V S V I T P G T N A S S
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT

590
 E V A V L Y Q D V N C T D V S
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT

600
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

610

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620
 S T G N N V F Q T Q A G C L I
 TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

630 640
 G A E H V D T S Y E C D I P I
 GGA GCT GAG CAT GTT GAT ACT TCT TAT GAG TGC GAC ATT CCT ATT

650
 G A G I C A S Y H T OC
 GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA TAA TGAGTCGAC
SEQ ID NO: 9799
SEQ ID NO: 9800

Translated Mol. Weight = 72525.52

FIGURE 66

1 10
 M S D L D R C T T F
 AAGCTTACAAAACAAA ATG AGT GAC CTT GAC CGG TGC ACC ACT TTT

20
 D D V Q A P N Y T Q H T S S M
 GAT GAT GTT CAA GCT CCT AAT TAC ACT CAA CAT ACT TCA TCT ATG

30 40
 R G V Y Y P D E I F R S D T L
 AGG GGG GTT TAC TAT CCT GAT GAA ATT TTT AGA TCA GAC ACT CTT

50
 Y L T Q D L F L P F Y S N V T
 TAT TTA ACT CAG GAT TTA TTT CTT CCA TTT TAT TCT AAT GTT ACA

60 70
 G F H T I N H T F G N P V I P
 GGG TTT CAT ACT ATT AAT CAT ACG TTT GGC AAC CCT GTC ATA CCT

80
 F K D G I Y F A A T E K S N V
 TTT AAG GAT GGT ATT TAT TTT GCT GCC ACA GAG AAA TCA AAT GTT

90 100
 V R G W V F G S T M N N K S Q
 GTC CGT GGT TGG GTT TTT GGT TCT ACC ATG AAC AAC AAG TCA CAG

110
 S V I I I N N S T N V V I R A
 TCG GTG ATT ATT ATT AAC AAT TCT ACT AAT GTT GTT ATA CGA GCA

120 130
 C N F E L C D N P F F A V S K
 TGT AAC TTT GAA TTG TGT GAC AAC CCT TTC TTT GCT GTT TCT AAA

140
 P M G T Q T H T M I F D N A F
 CCC ATG GGT ACA CAG ACA CAT ACT ATG ATA TTC GAT AAT GCA TTT

150 160
 N C T F E Y I S D A F S L D V
 AAT TGC ACT TTC GAG TAC ATA TCT GAT GCC TTT TCG CTT GAT GTT

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170
 S E K S G N F K H L R E F V F
 TCA GAA AAG TCA GGT AAT TTT AAA CAC TTA CGA GAG TTT GTG TTT
 180
 K N K D G F L Y V Y K G Y Q P
 AAA AAT AAA GAT GGG TTT CTC TAT GTT TAT AAG GGC TAT CAA CCT
 190
 200
 I D V V R D L P S G F N T L K
 ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA
 210
 P I F K L P L G I N I T N F R
 CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA
 220
 230
 A I L T A F S P A Q D I W G T
 GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG
 240
 S A A A Y F V G Y L K P T T F
 TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT
 250
 260
 M L K Y D E N G T I T D A V D
 ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT
 270
 C S Q N P L A E L K C S V K S
 TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC
 280
 290
 F E I D K G I Y Q T S N F R V
 TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT
 300
 V P S G D V V R F P N I T N L
 GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG
 310
 320
 C P F G E V F N A T K F P S V
 TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC
 330
 Y A W E R K K I S N C V A D Y
 TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC
 340
 350
 S V L Y N S T F F S T F K C Y
 TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT
 360
 G V S A T K L N D L C F S N V
 GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC
 370
 380
 Y A D S F V V K G D D V R Q I
 TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA
 390
 A P G Q T G V I A D Y N Y K L
 GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG
 400

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410
 P D D F M G C V L A W N T R N
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC
 420 430
 I D A T S T G N Y N Y K Y R Y
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT
 440
 L R H G K L R P F E R D I S N
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT
 450 460
 V P F S P D G K P C T P P A L
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT
 470
 N C Y W P L N D Y G F Y T T T
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT
 480 490
 G I G Y Q P Y R V V V L S F E
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA
 500
 L L N A P A T V C G P K L S T
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT
 510 520
 D L I K N Q C V N F N F N G L
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC
 530
 T G T G V L T P S S K R F Q P
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA
 540 550
 F Q Q F G R D V S D F T D S V
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT
 560
 R D P K T S E I L D I S P C S
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT
 570 580
 F G G V S V I T P G T N A S S
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT
 590
 E V A V L Y Q D V N C T D V S
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT
 600 610
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT
 620
 S T G N N V F Q T Q A G C L I
 TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA
 630 640
 G A E H V D T S Y E C D I P I

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GGA GCT GAG CAT GTC GAC ACT TCT TAT GAG TGC GAC ATT CCT ATT
 650
 G A G I C A S Y H T V S L L R
 GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA GTT TCT TTA TTA CGT
 660 670
 S T S Q K S I V A Y T M S L G
 AGT ACT AGC CAA AAA TCT ATT GTG GCT TAT ACT ATG TCT TTA GGT
 680
 A D S S I A Y S N N T I A I P
 GCT GAT AGT TCA ATT GCT TAC TCT AAT AAC ACC ATT GCT ATA CCT
 690 700
 T N F S I S I T T E V M P V S
 ACT AAC TTT TCA ATT AGC ATT ACT ACA GAA GTA ATG CCT GTT TCT
 710
 M A K T S V D C N M Y I C G D
 ATG GCT AAA ACC TCC GTA GAT TGT AAT ATG TAC ATC TGC GGA GAT
 720 730
 S T E C A N L L L Q Y G S F C
 TCT ACT GAA TGT GCT AAT TTG CTT CTC CAA TAT GGT AGC TTT TGC
 740
 T Q L N R A L S G I A A E Q D
 ACA CAA CTA AAT CGT GCA CTC TCA GGT ATT GCT GCT GAA CAG GAT
 750 760
 R N T R E V F A Q V K Q M Y K
 CGC AAC ACA CGT GAA GTG TTC GCT CAA GTC AAA CAA ATG TAC AAA
 770
 T P T L K Y F G G F N F S Q I
 ACC CCA ACT TTG AAA TAT TTT GGT GGT TTT AAT TTT TCA CAA ATA
 780 790
 L P D P L K P T K R S F I E D
 TTA CCT GAC CCT CTA AAG CCA ACT AAG AGG TCT TTT ATT GAG GAC
 800
 L L F N K V T L A D A G F M K
 TTG CTC TTT AAT AAG GTG ACA CTC GCT GAT GCT GGC TTC ATG AAG
 810 820
 Q Y G E C L G D I N A R D L I
 CAA TAT GGC GAA TGC CTA GGT GAT ATT AAT GCT AGG GAC CTC ATT
 830
 C A Q K F N G L T V L P P L L
 TGT GCG CAG AAG TTC AAT GGA CTT ACA GTG TTG CCA CCT CTG CTC
 840 850
 T D D M I A A Y T A A L V S G
 ACT GAT GAT ATG ATT GCT GCC TAC ACT GCT GCT CTA GTT AGT GGT
 860
 T A T A G W T F G A G A A L Q
 ACT GCC ACT GCT GGA TGG ACA TTT GGT GCT GGC GCT GCT CTT CAA
 870 880

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I P F A M Q M A Y R F N G I G
 ATA CCT TTT GCT ATG CAA ATG GCA TAT AGG TTC AAT GGC ATT GGA
 890
 V T Q N V L Y E N Q K Q I A N
 GTT ACC CAA AAT GTT CTC TAT GAG AAC CAA AAA CAA ATC GCC AAC
 900 910
 Q F N K A I S Q I Q E S L T T
 CAA TTT AAC AAG GCG ATT AGT CAA ATT CAA GAA TCA CTT ACA ACA
 920
 T S T A L G K L Q D V V N Q N
 ACA TCA ACT GCA TTG GGC AAG CTG CAA GAC GTT GTT AAC CAG AAT
 930 940
 A Q A L N T L V K Q L S S N F
 GCT CAA GCA TTA AAC ACA CTT GTT AAA CAA CTT AGC TCT AAT TTT
 950
 G A I S S V L N D I L S R L D
 GGT GCA ATT TCA AGT GTG CTA AAT GAT ATC CTT TCG CGA CTT GAT
 960 970
 K V E A E V Q I D R L I T G R
 AAA GTC GAG GCG GAG GTA CAA ATT GAC AGG TTA ATT ACA GGC AGA
 980
 L Q S L Q T Y V T Q Q L I R A
 CTT CAA AGC CTT CAA ACC TAT GTA ACA CAA CAA CTA ATC AGG GCT
 990 1000
 A E I R A S A N L A A T K M S
 GCT GAA ATC AGG GCT TCT GCT AAT CTT GCT GCT ACT AAA ATG TCT
 1010
 E C V L G Q S K R V D F C G K
 GAG TGT GTT CTT GGA CAA TCA AAA AGA GTT GAC TTT TGT GGA AAG
 1020 1030
 G Y H L M S F P Q A A P H G V
 GGC TAC CAC CTT ATG TCC TTC CCA CAA GCA GCC CCG CAT GGT GTT
 1040
 V F L H V T Y V P S Q E R N F
 GTC TTC CTA CAT GTC ACG TAT GTG CCA TCC CAG GAG AGG AAC TTC
 1050 1060
 T T A P A I C H E G K A Y F P
 ACC ACA GCG CCA GCA ATT TGT CAT GAA GGC AAA GCA TAC TTC CCT
 1070
 R E G V F V F N G T S W F I T
 CGT GAA GGT GTT TTT GTG TTT AAT GGC ACT TCT TGG TTT ATT ACA
 1080 1090
 Q R N F F S P Q I I T T D N T
 CAG AGG AAC TTC TTT TCT CCA CAA ATA ATT ACT ACA GAC AAT ACA
 1100
 F V S G N C D V V I G I I N N
 TTT GTC TCA GGA AAT TGT GAT GTC GTT ATT GGC ATC ATT AAC AAC

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```

      1110
T   V   Y   D   P   L   Q   P   E   L   D   S   F   K   E
ACA GTT TAT GAT CCT CTG CAA CCT GAG CTT GAC TCA TTC AAA GAA
      1120

E   L   D   K   Y   F   K   N   H   T   S   P   D   V   D
GAG CTG GAC AAG TAC TTC AAA AAT CAT ACA TCA CCA GAT GTT GAT
      1130

F   G   D   I   S   G   I   N   A   S   V   V   N   I   Q
TTT GGC GAC ATT TCA GGC ATT AAC GCT TCT GTC GTC AAC ATT CAA
      1140

K   E   I   D   R   L   N   E   V   A   K   N   L   N   E
AAA GAA ATT GAC CGC CTC AAT GAG GTC GCT AAA AAT TTA AAT GAA
      1150

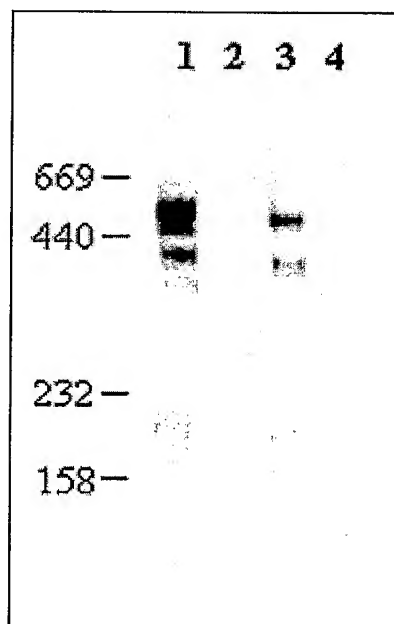
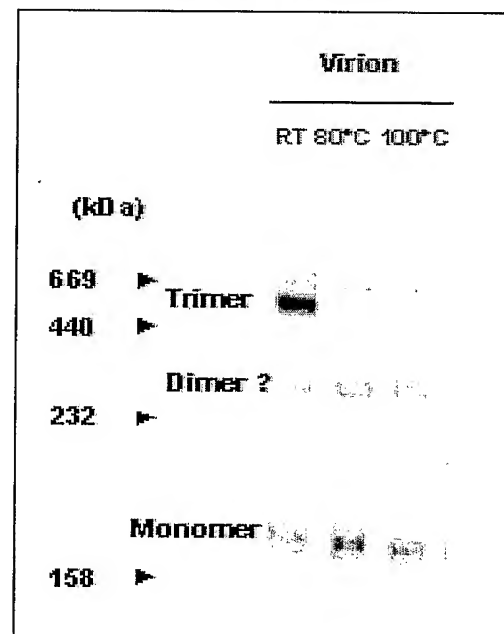
S   L   I   D   L   Q   E   L   G   K   Y   E   Q   Y   I
TCA CTC ATT GAC CTT CAA GAA TTG GGA AAA TAT GAG CAA TAT ATT
      1160

      1170
K   W   P   OC
AAA TGG CCT TAA TGAGTCGAC
      1180

```

Translated Mol. Weight = 131315.20

SEQ ID NO: 9801
SEQ ID NO: 9802

FIGURE 67**FIGURE 67A****FIGURE 67B**

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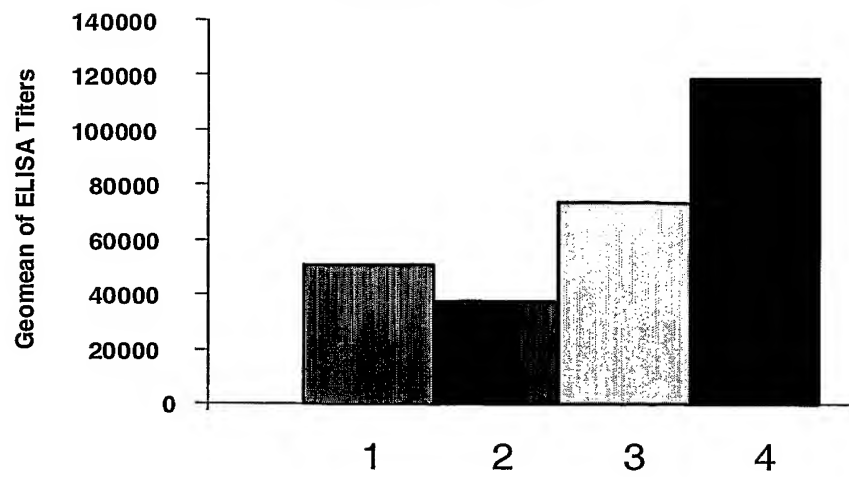
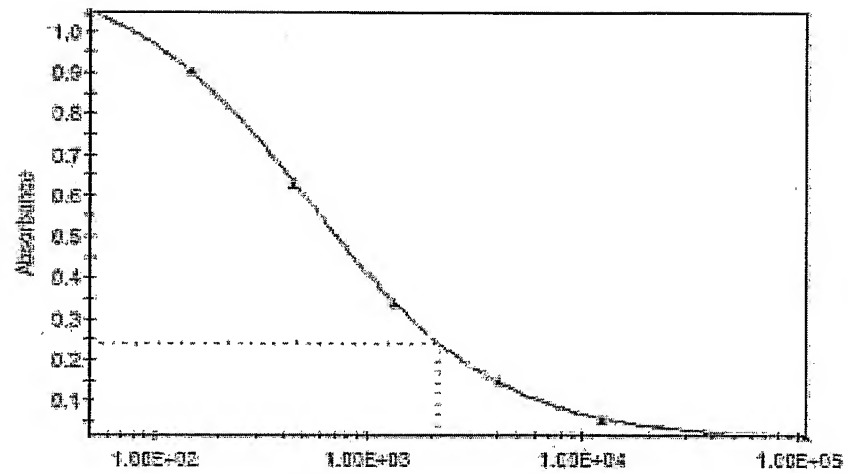
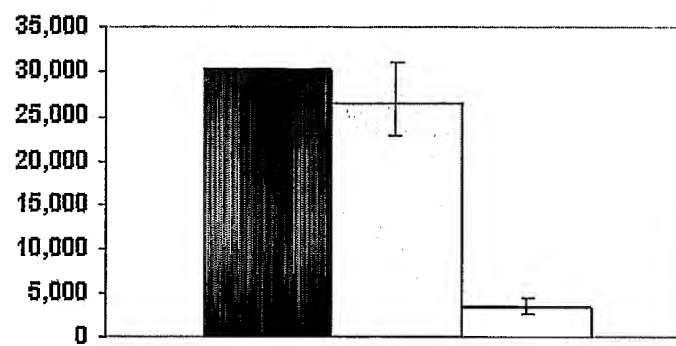
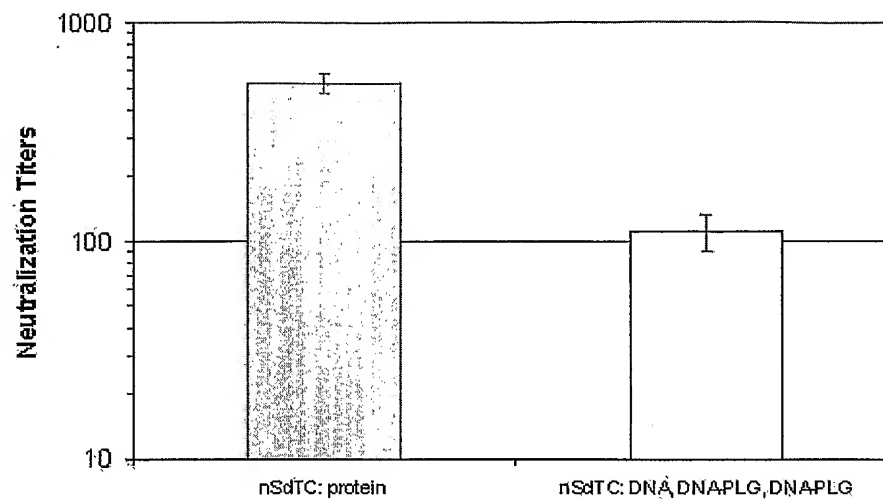
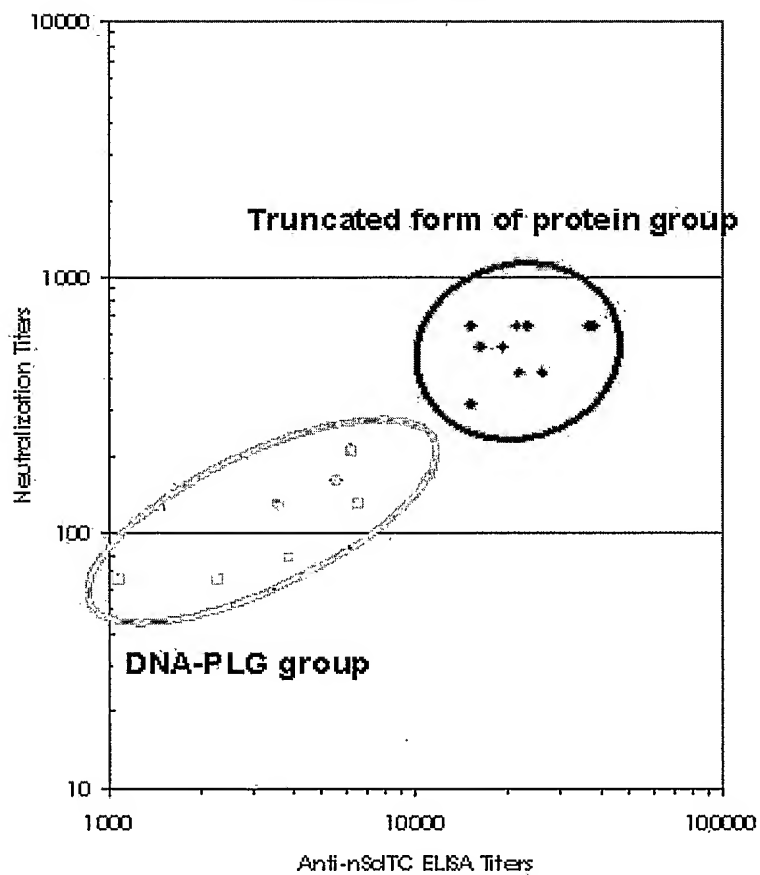
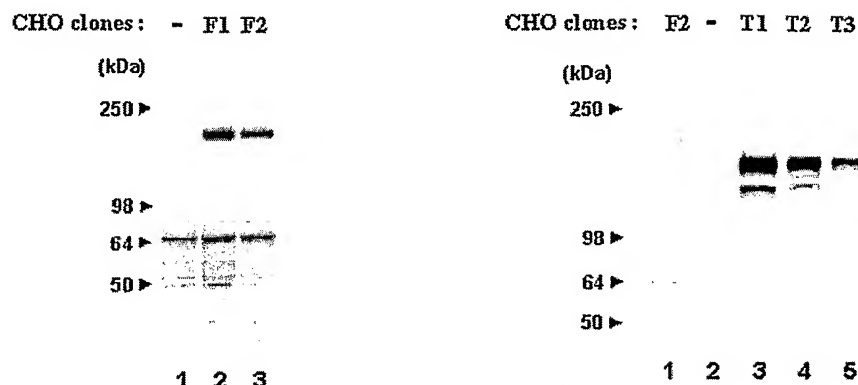
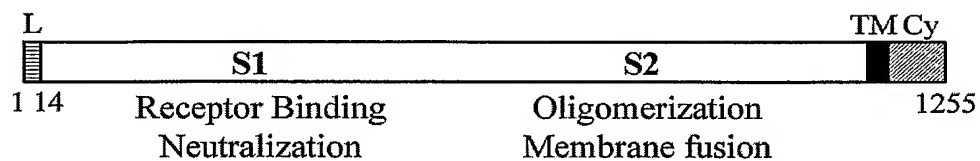
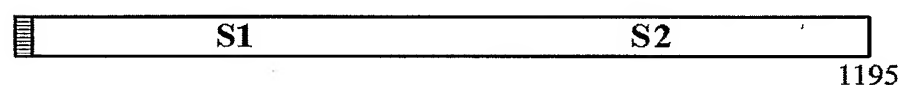
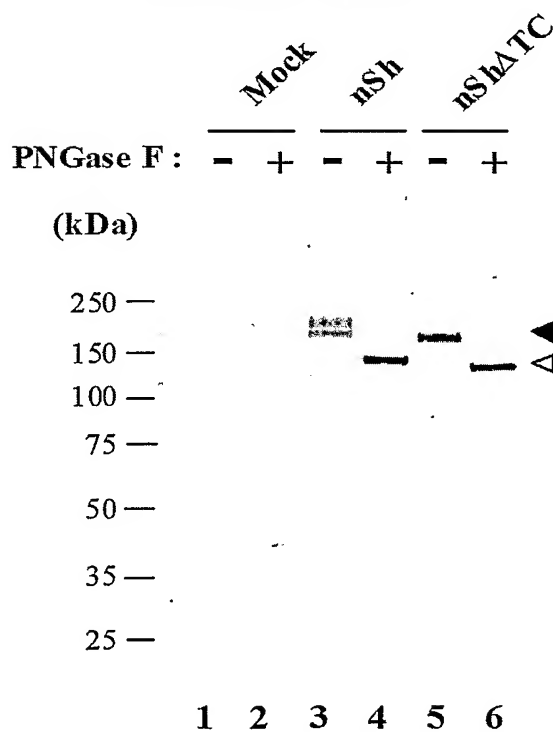
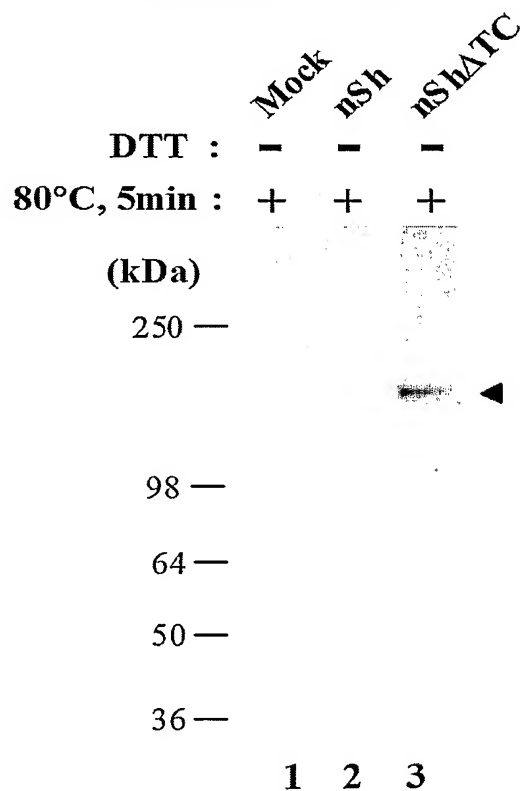
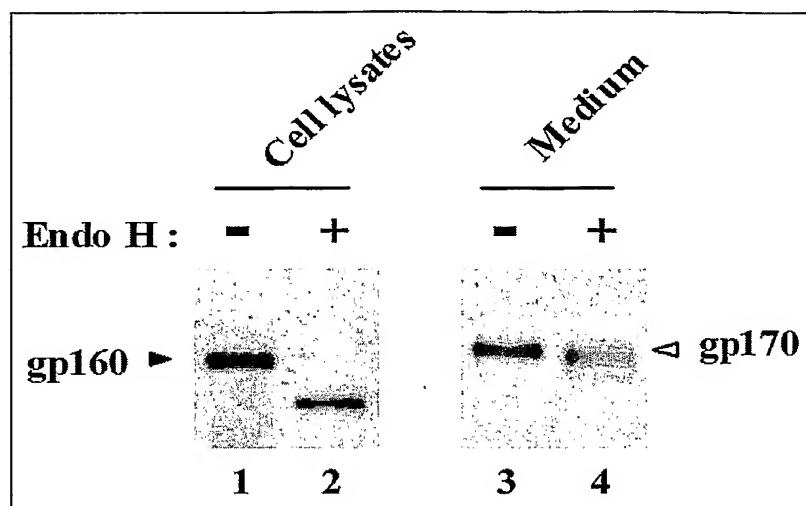
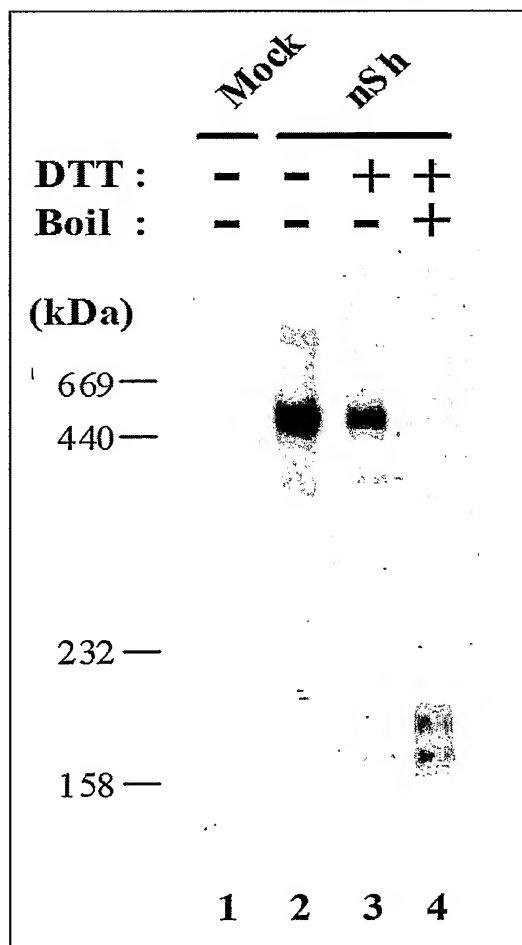
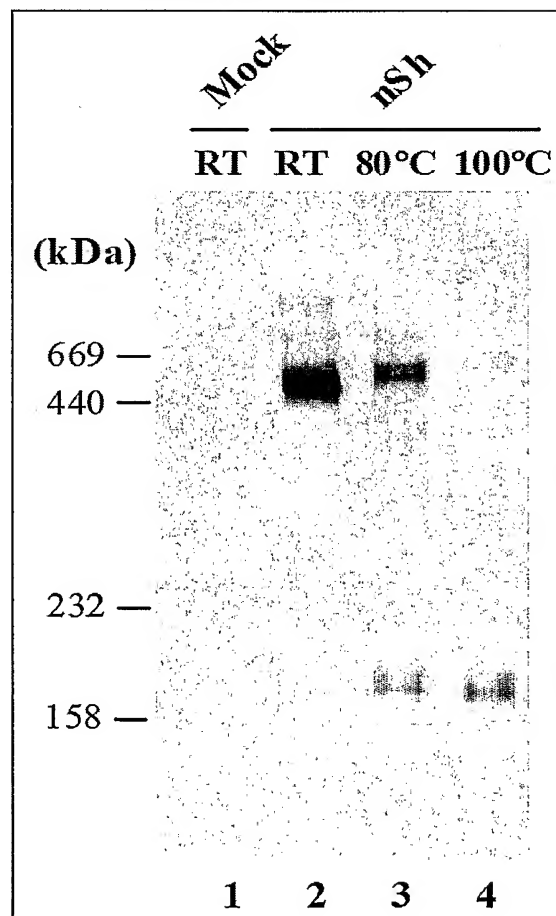
FIGURE 68**FIGURE 69****FIGURE 70**

FIGURE 71**FIGURE 72**

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FIGURE 73**FIGURE 74****FIGURE 74A****FIGURE 74B****FIGURE 75****FIGURE 75A****FIGURE 75B**

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FIGURE 76**FIGURE 77****FIGURE 78**

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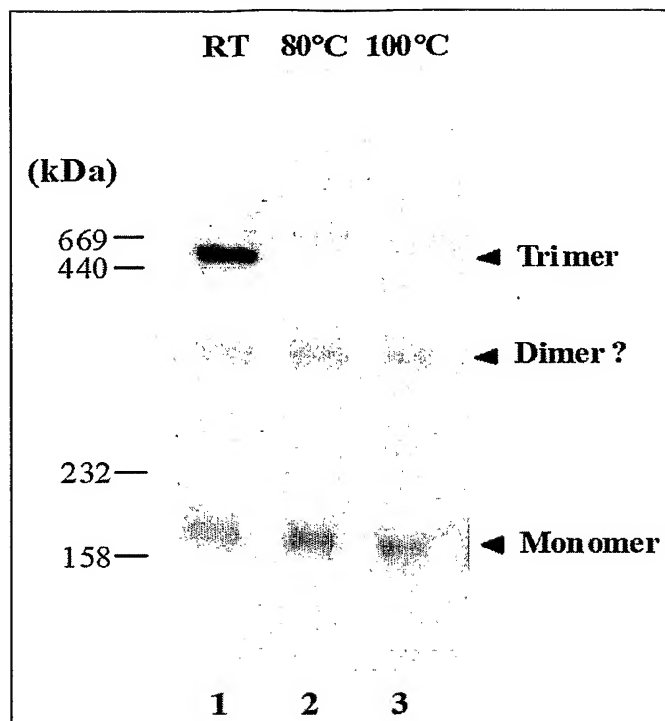
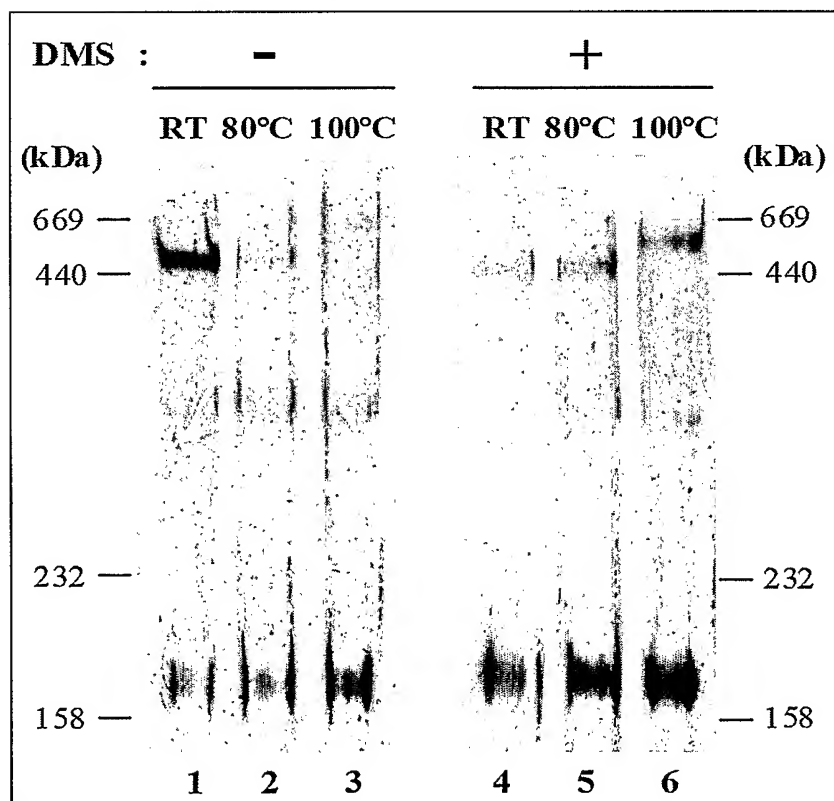
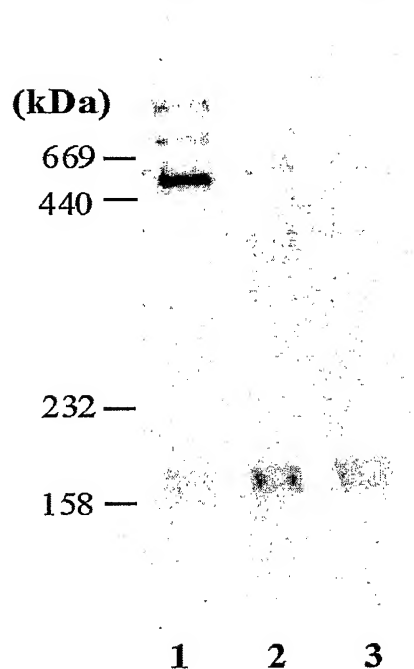
FIGURE 79**FIGURE 80**

FIGURE 81

RT 80°C 100°C

**FIGURE 82**

RT 80°C 100°C

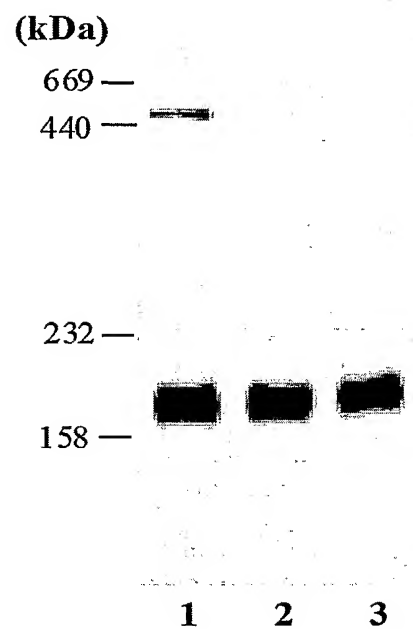
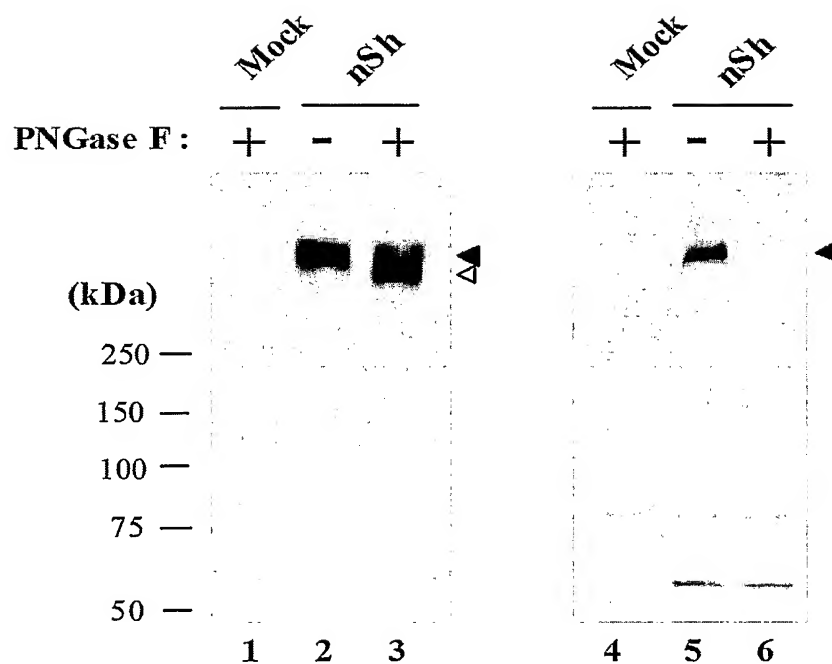
**FIGURE 83**

FIGURE 84

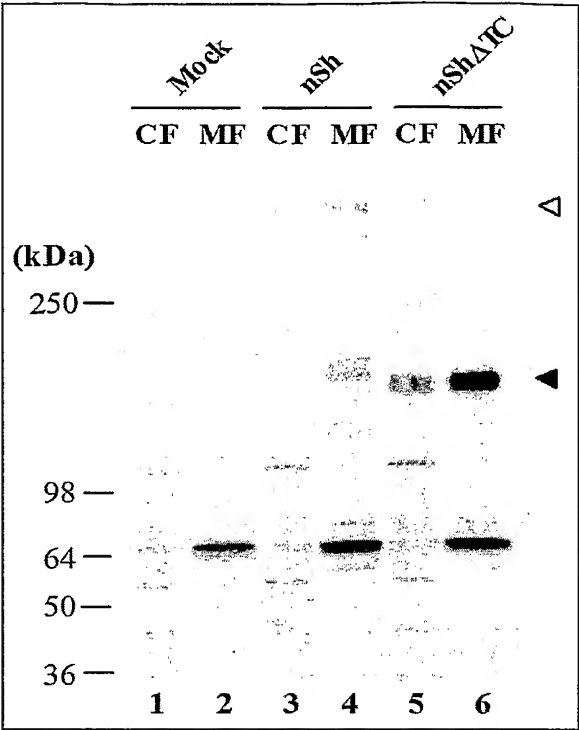


FIGURE 85

FIGURE 85A

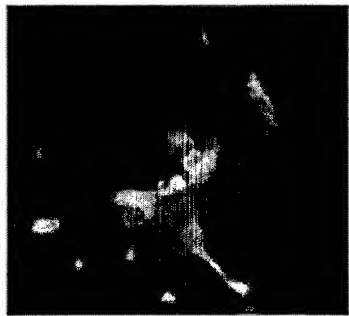


FIGURE 85B

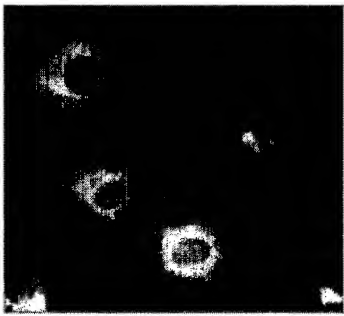


FIGURE 85C

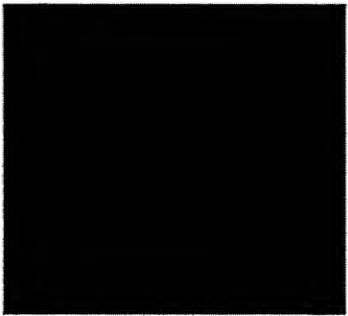


FIGURE 85D

FIGURE 85E

FIGURE 85F

FIGURE 86

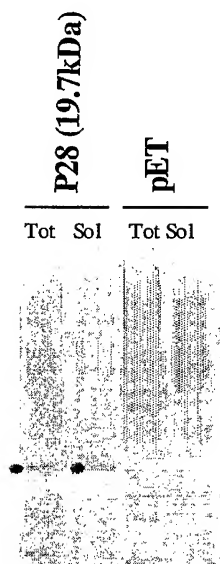


FIGURE 87

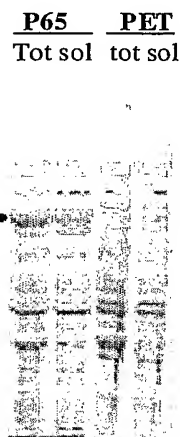


FIGURE 88

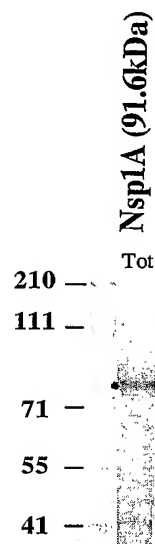


FIGURE 89

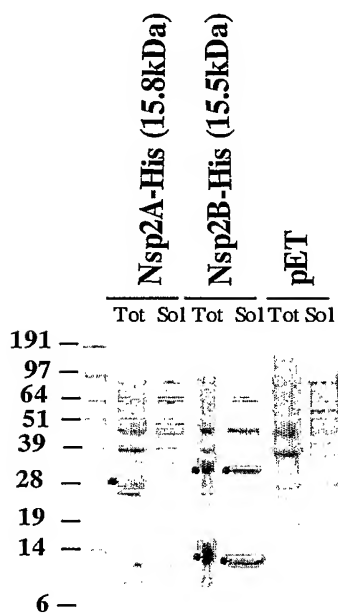


FIGURE 90

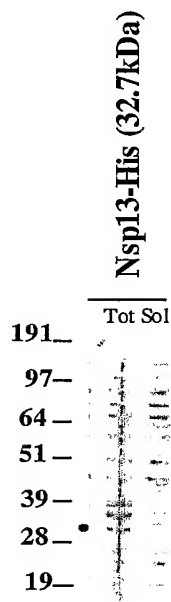


FIGURE 91

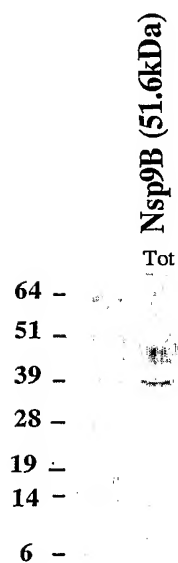


FIGURE 92

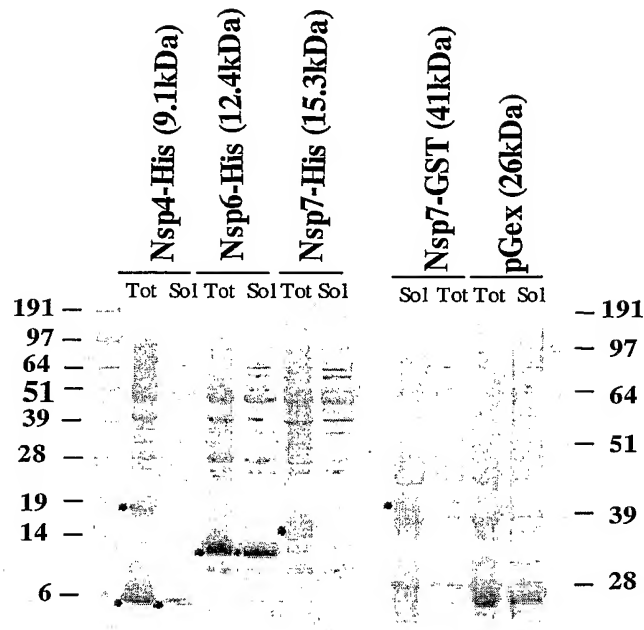


FIGURE 93

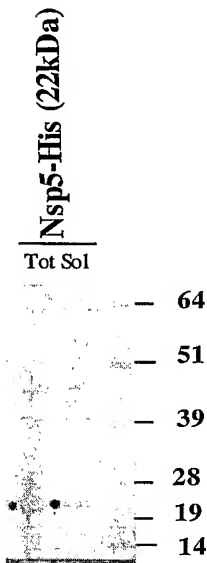


FIGURE 94

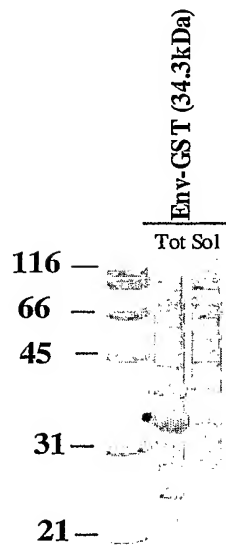


FIGURE 95

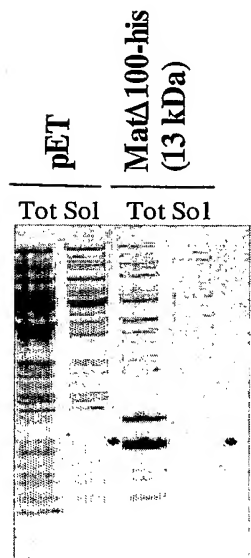


FIGURE 96

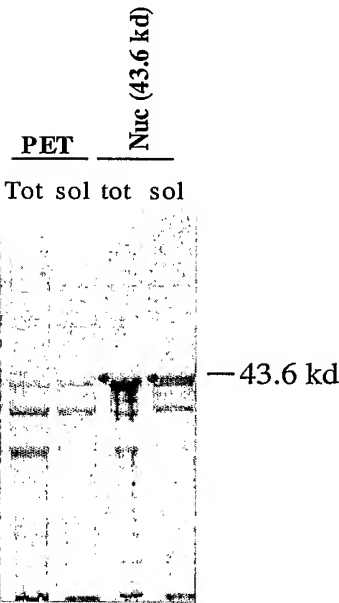


FIGURE 97

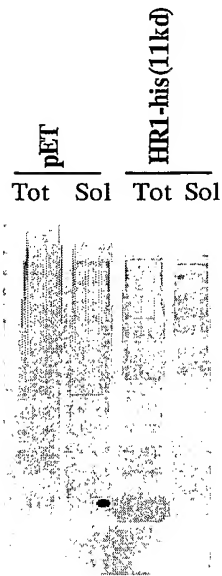


FIGURE 98

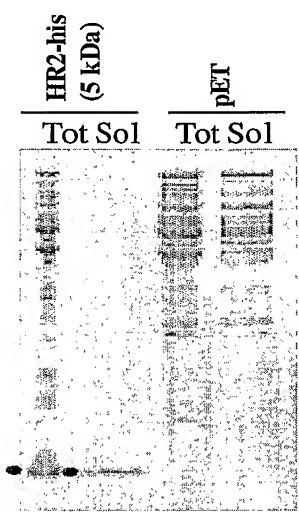


FIGURE 99

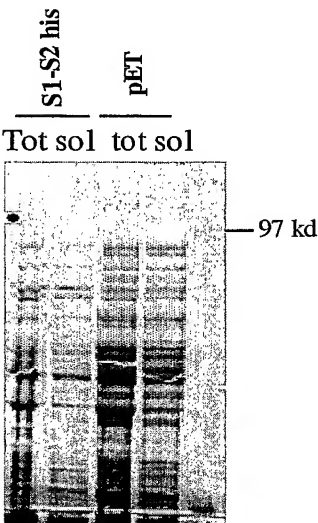


FIGURE 100

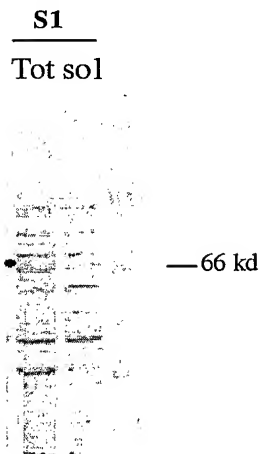


FIGURE 101

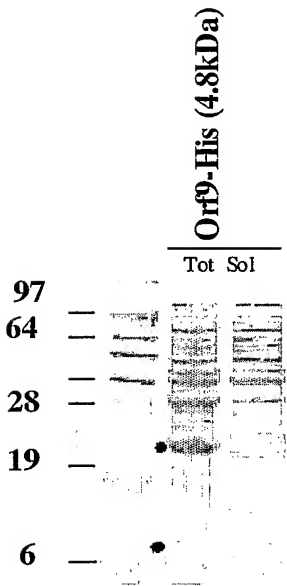


FIGURE 102

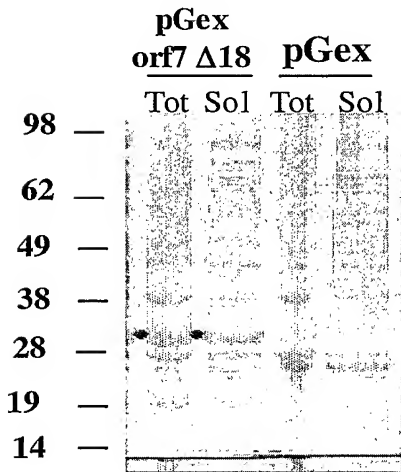


FIGURE 103

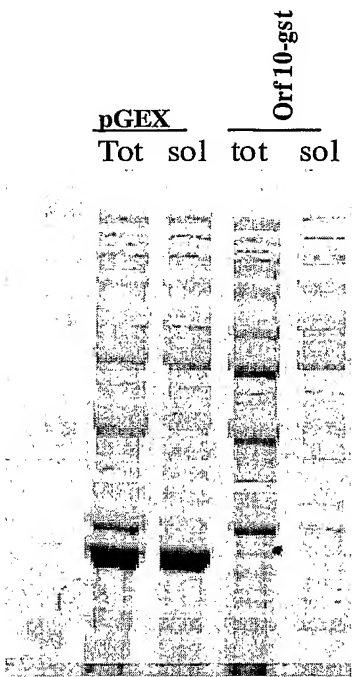


FIGURE 104

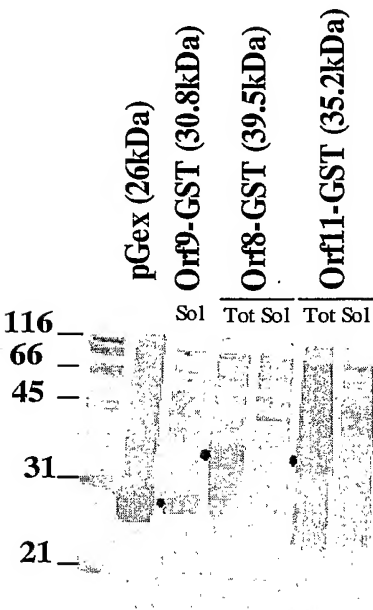


FIGURE 105

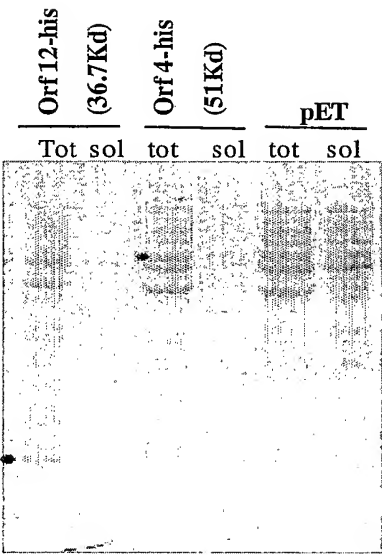


FIGURE 106

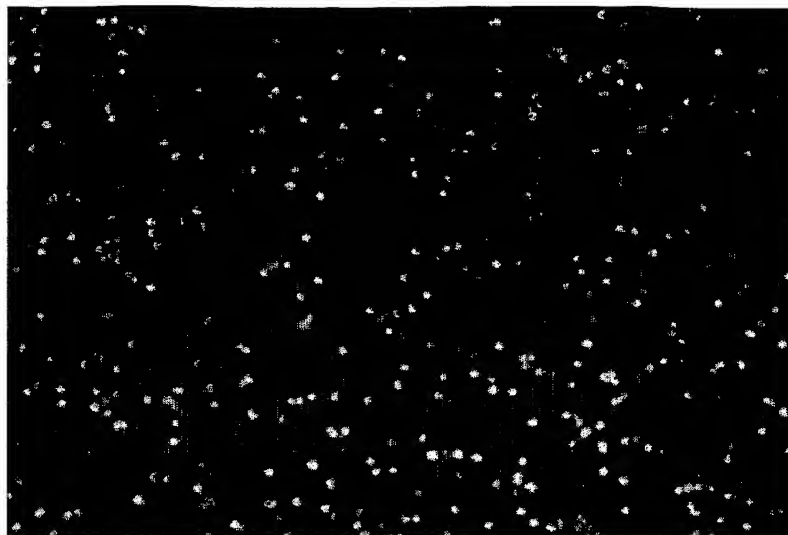


FIGURE 107

FIGURE 107A

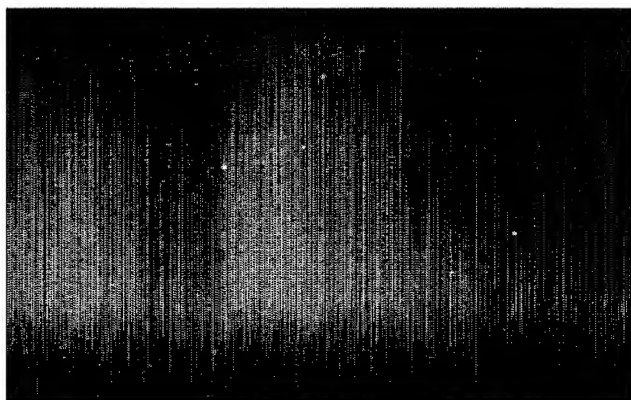


FIGURE 107B

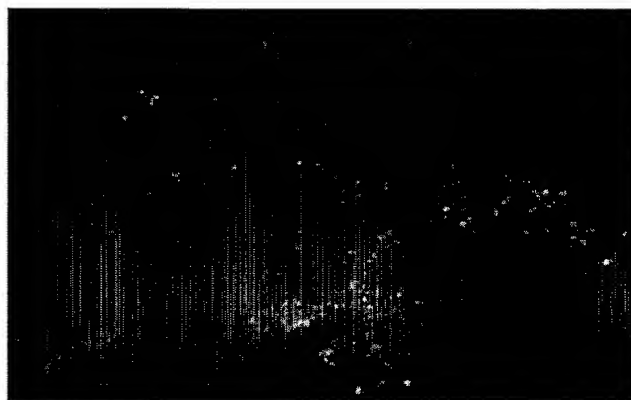


FIGURE 108

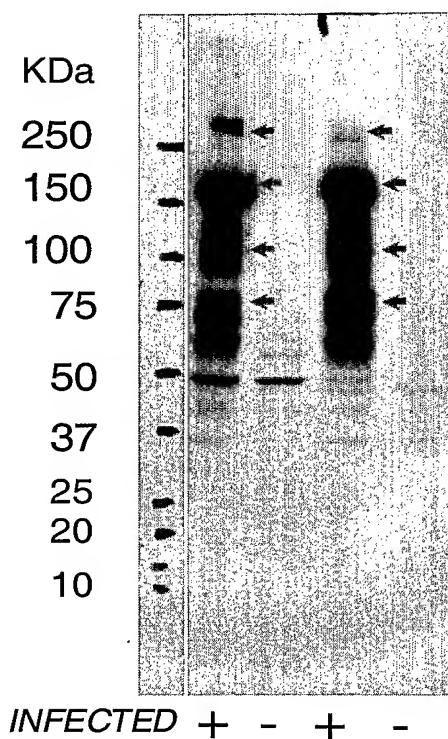
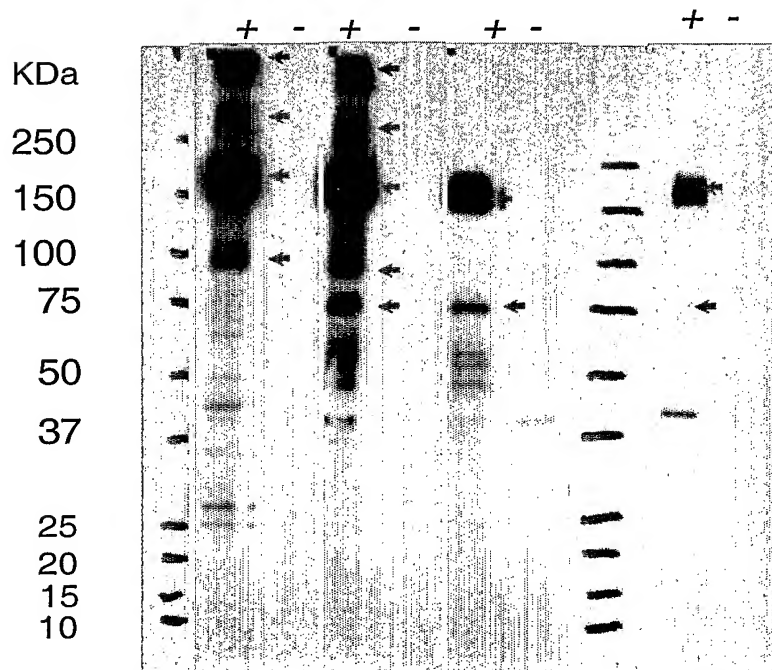
FIGURE 108A



FIGURE 108B



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FIGURE 109**S1 S1-S2****FIGURE 110****S1 S1-S2 HR2 HR1**

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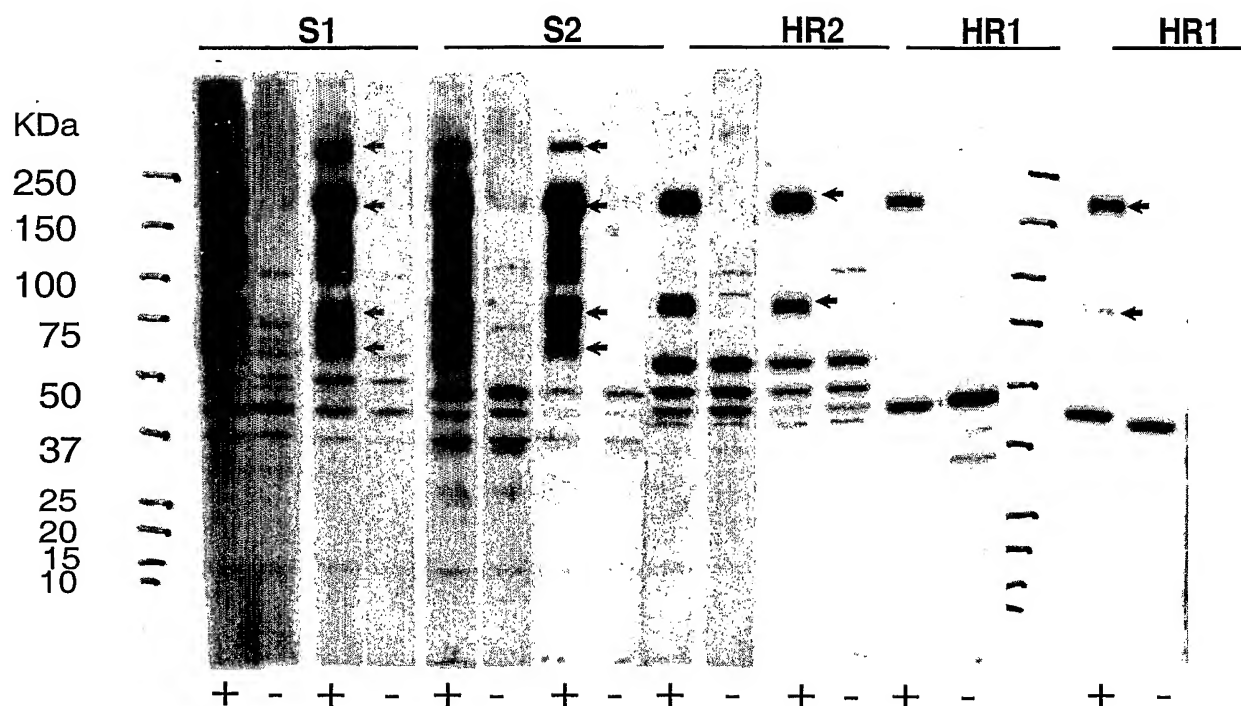
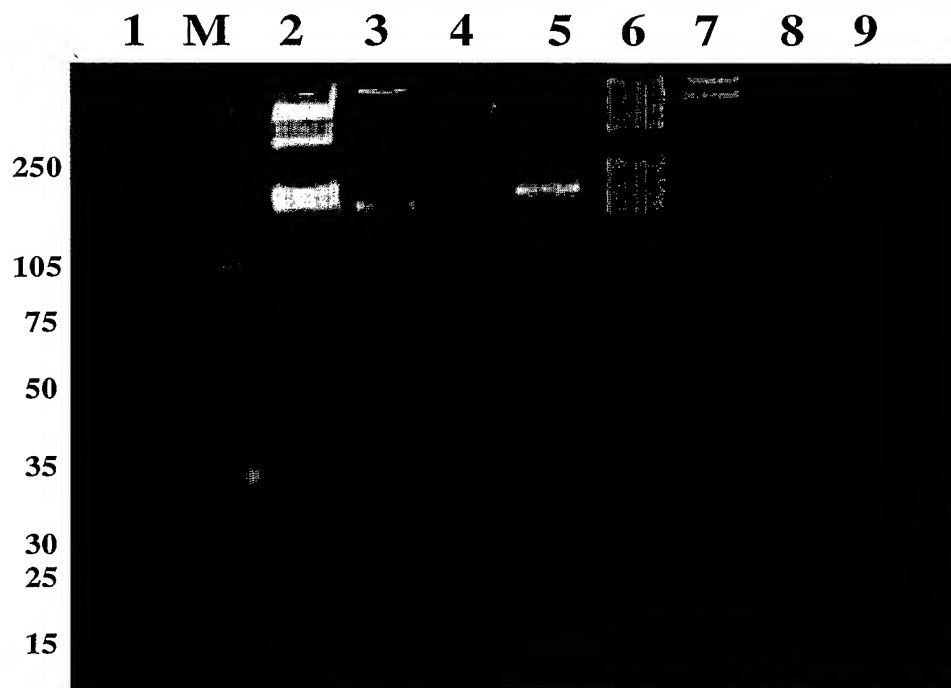
FIGURE 111**FIGURE 112**

FIGURE 113**5'3' Frame 1**

PKDMTYVDSSL-WVS-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYL
SS-DFLQVLT--LYRLVMLTLKITQNSPELMHKPPPVSLLNILYHSCIKACPGM-CVLR-
YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVCVTNVQLAFLHLHQILMPA
GIILWVL TMSITHL-LMFSSGGFTGNLSE-P-PTLPGTWKCTCGLVVML

5'3' Frame 2

QRT-PT-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PT
SPARIFYRC-LSSCTDWLC-H-K-HKIHQS-CTNLHQ-AV-TSYTTHV-RLALECSAY-D
STNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV-QTCNLLFYFIRYLCL
LESFCGF-LCL-PIYD-CSAVGALRVTFQSNHDQHCQVHGNAHVG-L-C

5'3' Frame 3

KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP
LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKI
VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC
WNHSVGFDYVYNPFMIDVQQWGLYG-PFRVTMTNIARYMEMHMMWASCA

3'5' Frame 1

-HHN-PTCAFPTWQCWSWLL-KVTRKAPTAEHQS-MGYRHSQNPQNDSSRHKYLK-KS
KLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-AFVLS-YALHSRAS
LYT-VV-DV-TAHWWRFVH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-L
HDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYVGHVLW

3'5' Frame 2

SITTSPHVHFHVPGNVGHGYSERLPVKPPLLNINHKWVIDIVKTHRMIPAGISI--SRKA
SCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITEHLYYLNTHYIPGQA
FIHEWYKMFKLLTGGLCINSGEFCVIFSVNITSRYSY-VNTRKS-LER-VSTHSISSC
MTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHRDEST-VMSF

3'5' Frame 3

ASQLAHMCISMYLAMLMVTLKGYP-SPHC-TSIINGL-T-SKPTE-FQQA-VSDEVEKQ
VARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTTSLDNPFVSVLSICTILIRTTFQGKP
LYMSGIRCLNCSLVEVCALTLVNFVLFVSVST-PVGTATKLTPVENPSWRGRLVPTASLVA
-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLRRSCPL

FIGURE 114**5'3' Frame 1**

YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLG
FSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLI

5'3' Frame 2

TVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-D
FLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSLNILY

5'3' Frame 3

P-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTSPARI
FYRC-LSSCTDWLC-H-K-HRIHQ5-CKTSTR-PV-TSYT

3'5' Frame 1

GIRCLNWSPGGGFALTLVNSVLF5VST-PVGTATKLTPVENPSWRGRLVPTASLVA-QPS
TSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR

3'5' Frame 2

V-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDSPL
HQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYG

3'5' Frame 3

YKMFKLVTWWRFCINSGEFCVIFSVNITSRY5Y-VNTCRKS-LER-VSTHSISSCMTALY
IKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDESTV

FIGURE 115**Section 151**

(5851) 5851 5860 5870 5889
 (5675) LTNVELSVINARIRAKHYVYIGDPAQLPAPRVLLSKGTL
 (5247) LTNVELSFINGKINYCYVVYVGDBAQLPAPRVLLING-ST
 (5762) LTNVELSVINSRYSARHYVYIGDPAQLPAPRVLLNEGTL
 (1) -----
 (5851) LTNVELSVINARI AKHYVYIGDPAQLPAPRVLLNKGTL

Section 152

(5890) 5890 5900 5910 5928
 (5714) EPKYENTVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (5285) SPKDYNVVTNLMVCVKPDIFLAKCYRCPKEIVDTVSTLV
 (5801) EPRYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (1) -----
 (5890) EPKYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV

Section 153

(5929) 5929 5940 5950 5967
 (5753) YDNKLKAKNDESSLGCFKVYYKG ---VTTHESSESAVNMQQ
 (5324) YDGNFIANNPESREGPKVIVNNGNSDVGHESGSAVNTTQ
 (5840) YDNKLKAKNDNSBMGCFKVYYKG ---QTTHESSESAVNMQQ
 (1) -----
 (5929) YDNKLKAKND SSLGCFKVYYKG TTHESSESAVNMQQ

Section 154

(5968) 5968 5980 5990 6006
 (5789) IYLLINKELKANPLWHKAVETSPYNSQNF AAKRVLGLQTO
 (5363) LEFVKDEVCRNKQWREAFISPYNAMNQRAYRMLGLNVQ
 (5876) IHLISKELKANPSWSNAVFISPYNSQNYVAKRVLGLQTO
 (1) -----
 (5968) IHLI KFLKANP W AVFISPYNSQNF AKRVLGLQTO

Section 155

(6007) 6007 6020 6030 6045
 (5828) TVDSAQGSSEYDYVIYSQTAETAHSVNVNRFNVAITRAKK
 (5402) TVDSSQGSSEYDYVIFCVTADSQHAIINRENVALTRAKE
 (5915) TVDSAQGSSEYDEVYIYSQTAETAHSVNVNRFNVAITRAKE
 (1) -----
 (6007) TVDSAQGSSEYDYVIYSQTAETAHSVNVNRFNVAITRAKK

Section 156

(6046) 6046 6060 6070 6084
 (5867) GILCVMSNMQLFEALQFTTTLTLDKVPQAVETRVQCSTNL
 (5441) GILVVMRQRDELYSALKFTELDSETS ----LQG--TEL
 (5954) GILCVMSNMQLFESLNFTTTLTLDKIN ---NPRLOCTTNL
 (1) -----
 (6046) GILCVMSNMQLFESLNFTTTLTLDKI RLQCSTNL

START

FIGURE 115 (contd.)**Section 157**

(6085) 6085 6090 6100 6110 6123
 (5906) FKDCSKSYSGYHPAHAPSFLAVDDKYKATGDLAVELGIG
 (5473) EKICCKEFSGVHPAYAVTTKALAAATYKVNDELAPLYNVE
 (5990) EKDCSRSEYVGYPAHAPSFLAVDDKYKVGCDLAVCLNVA
 (1) -----
 (6085) FKDCSKSYSGYHPAHAPSFLAVDDKYKV GDLAVCLNVA

Section 158

(6124) 6124 6130 6140 6150 6162
 (5945) D-SAVTYSRLSENGTLDVLDYCHL-LIKEH-VKR
 (5512) AGSETTYRHL-LLFIMSVIVE-CHNM-TRDEAIRN
 (6029) D-SAVTYSRLHIMC-LDLTLD-YCHL-TRDEAIRN
 (1) --KGHDLRP-CHM-FIMSYQV-YENM-TRDEAIRN
 (6124) D SAVTYSRLISLMGFKLDVTLDGYCNLFITRDEAIKRV

Section 159

(6163) 6163 6170 6180 6190 6201
 (5983) RAIVTDFRGAH-TRDSIT-TNFSLD-TRD-IDEVVEAT
 (5551) RG-V-EDVEATE-EGTNTSLPL-TRDA-IDEVVEAT
 (6067) RAIVTDFRGAH-TRDSIT-TNFSLD-TRD-IDEVVEAT
 (38) RAIVTDFRGAH-TRDAVGT-TNFSLD-TRD-IDEVVEAT
 (6163) RANVGFDVEGAHATRDSIGTNLPLQLGESTGIDEVVEPT

Section 160

(6202) 6202 6210 6220 6230 6240
 (6022) GLFADRDGYSEKKAVAKAPPGEQFKHLIPLMSRGPWDV
 (5590) GLVDTRDGYSEKPVNSKAPPGEQFKHLIPLMSRGPWDV
 (6106) GLFADRDGYSEKKAAARAPPGEQFKHLIPLMSRGPWDV
 (77) GLVDTRDGYSEKPVNSKAPPGEQFKHLIPLMSRGPWDV
 (6202) GLVDTRDGY FKKVNAKAPPGEQFKHLIPLMSRGPWDV

Section 161

(6241) 6241 6250 6260 6279
 (6061) VRPRIVQMLADHLIDLSDCVVLVTWAHGFELTCLRYFVK
 (5629) VRPRIVQMLADHLIDLSDCVVLVTWAHGFELTCLRYFVK
 (6145) VRPRIVQMLADHLIDLSDCVVLVTWAHGFELTCLRYFVK
 (116) VRPRIVQMLADHLIDLSDCVVLVTWAHGFELTCLRYFVK
 (6241) VRPRIVQMLADHL DLSDCVVLVTWAHGFELTCLRYFVK

Section 162

(6280) 6280 6290 6300 6318
 (6100) VGRISCNVCTKRATCFNSRTGYGACWRHSVTCYLYNP
 (5668) IGRK-OVCS-IGGAT-TENSHTQAYACWKHCLGFLFVNH
 (6184) VGRVVDSEVTKRATCFNSRTGYGACWRHSVTCYLYNP
 (155) IGRPERTEGLIDKFAIGFSTSSCTVACWHSVTCYLYNP
 (6280) IGRISCCVCTKRATCFNSRTGYGACWRHSVTCYLYNP

FIGURE 115 (contd.)**Section 163**

| | | | | |
|--------|---|------|------|------|
| (6319) | 6319 | 6330 | 6340 | 6357 |
| (6139) | LIVDIQCFEYICSLSSNHDLYCSVHKGAHVASSDAIMTR | | | |
| (5706) | LLVLIKQNYISGNLOFNHDLHCNVHGHAHVASVDAIMTR | | | |
| (6223) | LIVDIQCFEYICSLSSNHDLYCSVHKGAHVASSDAIMTR | | | |
| (194) | FMIDVQCFEYICSLSSNHDLYCSVHKGAHVASSDAIMTR | | | |
| (6319) | LIVDIQCFEYICSLSSNHDLYCSVHKGAHVASSDAIMTR | | | |

Section 164

| | | | | |
|--------|---|------|------|------|
| (6358) | 6358 | 6370 | 6380 | 6396 |
| (6178) | CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL | | | |
| (5745) | CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL | | | |
| (6262) | CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL | | | |
| (229) | ----- | | | |
| (6358) | CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL | | | |

Section 165

| | | | | |
|--------|--|------|------|------|
| (6397) | 6397 | 6410 | 6420 | 6435 |
| (6217) | KAAMLCNRYTLCYDIGNPKAIACVKD--EDEFKEYDAOPT | | | |
| (5784) | NACVDALKVNVVYDIGNPKGIKCVRRGDVNEREFYDKNEI | | | |
| (6301) | KAAMLCNRYTLCYDIGNPKAIACVKD--EDEFKEYDAOPT | | | |
| (229) | ----- | | | |
| (6397) | KAAMLCNRYTLCYDIGNPKAIACVKD--EDEFKEYDAOPT | | | |

Section 166

| | | | | |
|--------|---|------|------|------|
| (6436) | 6436 | 6450 | 6460 | 6474 |
| (6254) | VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAV | | | |
| (5823) | VRNVKQFEYDYNQHKDKFADGLCMFWNCNVDPKYPNAV | | | |
| (6338) | VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAV | | | |
| (229) | ----- | | | |
| (6436) | VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAV | | | |

Section 167

| | | | | | |
|--------|---|------|------|------|------|
| (6475) | 6475 | 6480 | 6490 | 6500 | 6513 |
| (6293) | CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE | | | | |
| (5862) | CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE | | | | |
| (6377) | CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE | | | | |
| (229) | ----- | | | | |
| (6475) | CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE | | | | |

Section 168

| | | | | | |
|--------|--|------|------|------|------|
| (6514) | 6514 | 6520 | 6530 | 6540 | 6552 |
| (6332) | NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR | | | | |
| (5901) | NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR | | | | |
| (6416) | NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR | | | | |
| (229) | ----- | | | | |
| (6514) | NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR | | | | |

FIGURE 115 (contd.)

Section 169

| | | | | | |
|--------|--|------|------|------|------|
| (6553) | 6553 | 6560 | 6570 | 6580 | 6591 |
| (6371) | CNIGGAVCLKHAEFYREYLESYNTATTAGFTFWVYKTFD | | | | |
| (5939) | CNIGGAVCKKHAQMYAEFWTSYNAAVTAGFTFWVTHL LN | | | | |
| (6455) | CNLGGAVCLKHAEFYREYLESYNTATTAGFTFWVYKTFD | | | | |
| (229) | ----- | | | | |
| (6553) | CNLGGAVCLKHAEFYREYLESYNTATTAGFTFWVYKTFD | | | | |

Section 170

| | | | | | |
|--------|--|------|------|------|------|
| (6592) | 6592 | 6600 | 6610 | 6620 | 6630 |
| (6410) | FYNLWNTFTKLOSLENNVYNLVKTGHYTGQAGEMPCAII | | | | |
| (5978) | PYNLWKSEFSALOSIDNIAYNMYKGCHYDAIAGEMPTVIT | | | | |
| (6494) | FYNLWNTFTRLLOSLENNVYNLVNAGHFDGRAGELPCAII | | | | |
| (229) | ----- | | | | |
| (6592) | FYNLWNTFTKLOSLENNVYNLVKAGHYDG AGEMPCAII | | | | |

Section 171

| | | | | |
|--------|---|------|------|------|
| (6631) | 6631 | 6640 | 6650 | 6669 |
| (6449) | GDKVVAKIDKEDVVFINTTPTNVAVELFAKRSTRHH | | | |
| (6017) | GDKVVFVIDQGVKAVFVNQTTLPSTVAFELYAKRNIRTL | | | |
| (6533) | GERVIAKIQNEDEVVVEKNNTTPTNVAVELFAKRSTRPH | | | |
| (229) | ----- | | | |
| (6631) | GDKVIAKIQ EDVVVFINTTPTNVAVELFAKRSIR H | | | |

Section 172

| | | | | |
|--------|---|------|------|------|
| (6670) | 6670 | 6680 | 6690 | 6708 |
| (6488) | PELKLFRNLNIDVCWKHVIWDYARESTFCSNTYGVCMYT | | | |
| (6056) | ENNRLKGLGVDTNGFVIWDYALCTPIYRNTYKVCANT | | | |
| (6572) | PELKLFRNLNIDVCWSHVLWDYAKDSVECSSTYKVCXYT | | | |
| (229) | ----- | | | |
| (6670) | PELKLFRNLNIDVCW HVIWDYAKDSIFCSNTYKVC YT | | | |

Section 173

| | | | | |
|--------|--|------|------|------|
| (6709) | 6709 | 6720 | 6730 | 6747 |
| (6527) | DLKFFDKLNVLFEDGRDNGALEAFKRSNNGVYISTTKVKS | | | |
| (6095) | DIEPNG--LVVLYDDPYGDYCSFLAADNAVLMSTQCCKR | | | |
| (6611) | DLQCFESLNVLFEDGRDNGALEAFKRSNNGVYINTTKIKS | | | |
| (229) | ----- | | | |
| (6709) | DL ID LNVLFEDGRDNGALEAFKKA NGVYISTTKIKS | | | |

Section 174

| | | | | |
|--------|--|------|------|------|
| (6748) | 6748 | 6760 | 6770 | 6786 |
| (6566) | LSMIKGPRAELNGVVVDKVGSDTDCVFFFAVRKEGQDVI | | | |
| (6132) | YSYVEIPSLLVQNGMPLKDG-----ANLYV | | | |
| (6650) | LSMIKGPORADLNGVVVEKVGSDSDFEFWFAVRKDGNDVI | | | |
| (229) | ----- | | | |
| (6748) | LSMIKGP RADLNGVVVDKVGSD FWFVRKDGNDVI | | | |

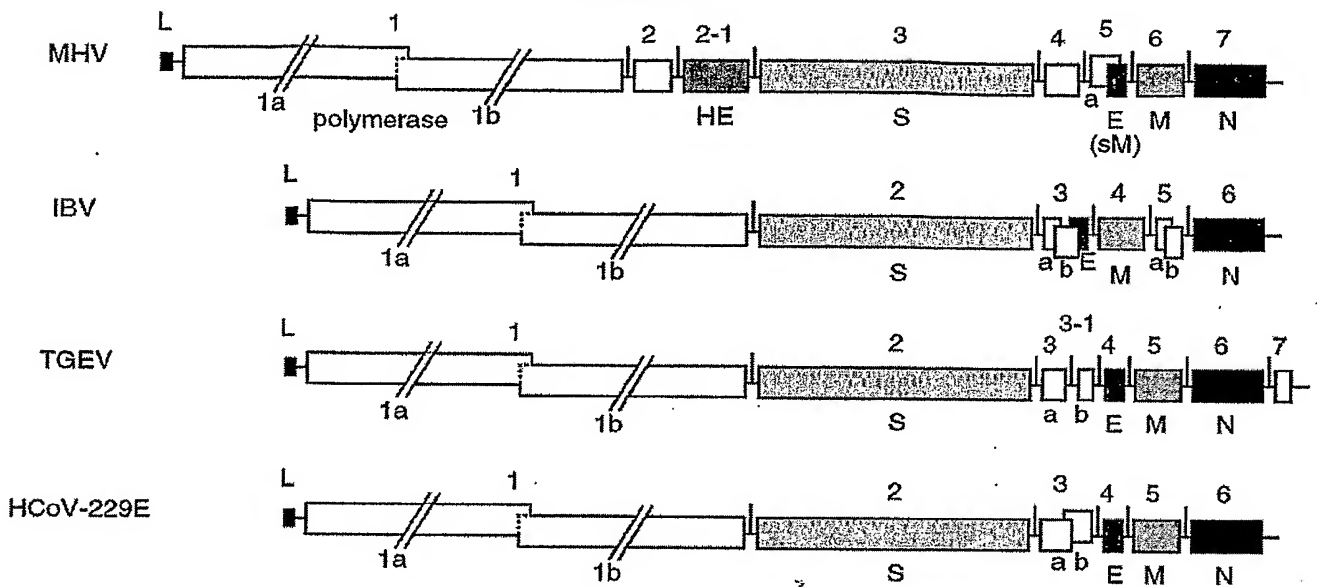
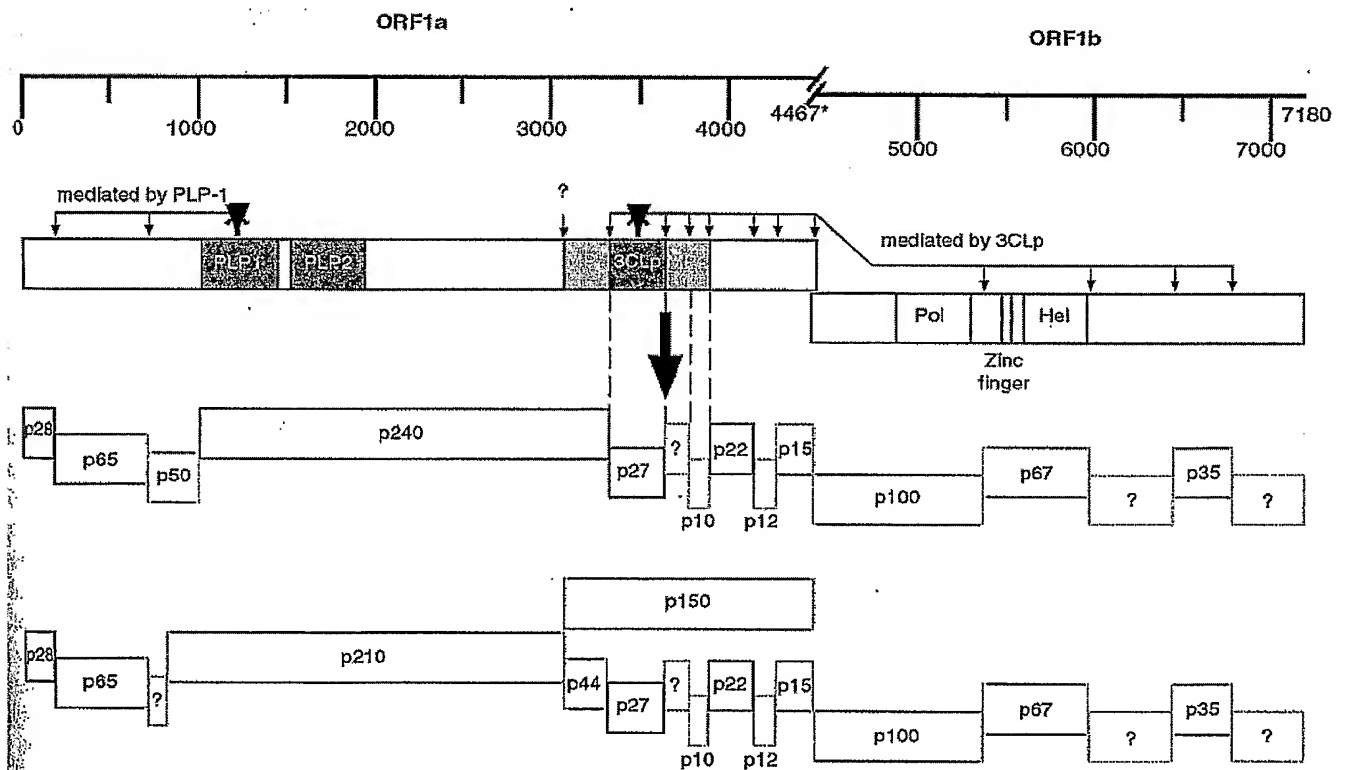
SEQ ID NO: 10068

SEQ ID NO: 10069

SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

FIGURE 116**FIGURE 117**

“*”

FIGURE 118

| Section 1 | | | | | |
|-----------|---|-----|-----|-----|-----|
| (1) | 1 | 10 | 20 | 30 | 40 |
| (1) | -GAGGIFKIQNKEEFGVHPYVVTTRKLAATGVNDELALVNVEAGKSAFV | | | | |
| (1) | CSTNLFEDSKSYSYPAHPSFLVDDKFRATGDLVCLCIGD-KHPT | | | | |
| (1) | CTTNLFEDSRSYVLYHPAHPSFLVDDKLVGGDLVCLNVAD-KOHL | | | | |
| (1) | CSTNLFEDSKSYSYPAHPSFLVDDKLVGGDLVCLNVAD-KHPT | | | | |
| (1) | CSTNLFKDCSKSYSGYHPAHAPSFLAVDDKYKVGGDLAVCLNVAD KGHDL | | | | |
| Section 2 | | | | | |
| (52) | 52 | 60 | 70 | 80 | 90 |
| (51) | RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG | | | | |
| (51) | RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG | | | | |
| (51) | RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG | | | | |
| (51) | RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG | | | | |
| (52) | RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG | | | | |
| Section 3 | | | | | |
| (103) | 103 | 110 | 120 | 130 | 140 |
| (102) | TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM | | | | |
| (102) | TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM | | | | |
| (102) | TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM | | | | |
| (102) | TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM | | | | |
| (103) | TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM | | | | |
| Section 4 | | | | | |
| (154) | 154 | 160 | 170 | 180 | 190 |
| (153) | YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE | | | | |
| (153) | YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE | | | | |
| (153) | YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE | | | | |
| (153) | YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE | | | | |
| (154) | YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE | | | | |
| Section 5 | | | | | |
| (205) | 205 | 210 | 220 | 230 | 240 |
| (204) | RTCCLCDKCRATCFSTSSDTYACWNHSGEDYVYNPFMIDVQQWGLYGSLS | | | | |
| (204) | RTCCLCDKCRATCFSTSSDTYACWNHSGEDYVYNPFMIDVQQWGLYGSLS | | | | |
| (204) | RTCCLCDKCRATCFSTSSDTYACWNHSGEDYVYNPFMIDVQQWGLYGSLS | | | | |
| (204) | RTCCLCDKCRATCFSTSSDTYACWNHSGEDYVYNPFMIDVQQWGLYGSLS | | | | |
| (205) | RTCCLCDKCRATCFSTSSDTYACWNHSGEDYVYNPFMIDVQQWGLYGSLS | | | | |
| Section 6 | | | | | |
| (256) | 256 | 270 | 280 | 290 | 306 |
| (255) | NHDHLHCSVHKGAVHVAASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN | | | | |
| (255) | NHDLYCSVHKGAVHVAASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN | | | | |
| (255) | NHDPICSVHKGAVHVAASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN | | | | |
| (255) | NHDHLHCSVHKGAVHVAASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN | | | | |
| (256) | NHDHLHCSVHKGAVHVAASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN | | | | |

FIGURE 118 (contd.)**Section 7**

| | | | | |
|---|-----|-----|----------------|-----|
| (307) 307 | 320 | 330 | 340 | 357 |
| (306) SPTFYLLSEMYLNALMDALKVNVVLEDPAGLKVRRGQVNTERTTEKNEIA | | | | |
| (306) TSCSVLLSEVMLKAAMLCNRETLCYDIGNPKAIACVK--DFDEKFIYDAQEIV | | | | |
| (306) TSCVLLSEVMLKAAMLCNRYDVCCDIGNPKGLACVK--GYDEKFIYDAEIV | | | | |
| (306) TSCVLLSEVMLKAAMLCNRYTVCCDIGNPKGLACVK--DFDETKFIYDAEIV | | | | |
| (307) TSCRLLRVMLKAAMLCNRYTVCYDIGNPKGIACVK | | | DFDEKFIYDANPIV | |

Section 8

| | | | | |
|---|-----|-----|-----|-----|
| (358) 358 | 370 | 380 | 390 | 408 |
| (357) RNVKQFELYDYNQHKDKFADGLCMFWNCNVDCYFDNSLVCRDYDTPNLSVFNL | | | | |
| (355) KSVKTLLYSFEAHKDSFKDGLCMFWNCNVDKYFPNAVVCREDTRVLNNLNL | | | | |
| (355) KSVKQFVYKYEAHKDQFLDGLCMFWNCNVDKYPANAVVCREDTRVLNKLNL | | | | |
| (355) KSVKQELYSYEAHKDSFKDGLCMFWNCNVDKYPANAVVCREDTRVLN-LNL | | | | |
| (358) KSVKQFLYSYEAHKDSFKDGLCMFWNCNVDKYPANAVVCREDTRVLN | | | | LNL |

Section 9

| | | | | |
|---|-----|-----|-----|-----|
| (409) 409 | 420 | 430 | 440 | 459 |
| (408) PGCNGGSLYVNHAFHTKPKFSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ | | | | |
| (406) PGCNGGSLYVNHAFHTKPKFSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ | | | | |
| (406) PGCNGGSLYVNHAFHTKPKFSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ | | | | |
| (405) PGCNGGSLYVNHAFHTKPKFSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ | | | | |
| (409) PGCNGGSLYVNHAFHTKPKFSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ | | | | |

Section 10

| | | | | | |
|---|-----|-----|-----|-----|-----|
| (460) 460 | 470 | 480 | 490 | 500 | 510 |
| (458) QVLYSLATKDEITKCHTGGAVCLKHAAEYREYLESYNTATTAGFTFWVYKT | | | | | |
| (457) VDYVPLKSATCITRCNLGGAVCLKHAAEYREYLESYNTATTAGFTFWVYKT | | | | | |
| (457) VDYVPLKSATCITRCNLGGAVCLKHAAEYREYLESYNTATTAGFTFWVYKT | | | | | |
| (456) VDYVPLKSATCITRCNLGGAVCLKHAAEYREYLESYNTATTAGFTFWVYKT | | | | | |
| (460) VDYVPLKSATCITRCNLGGAVCLKHAAEYREYLESYNTATTAGFTFWVYKT | | | | | |

Section 11

| | | |
|----------------------|------------------|--|
| (511) 511 | 524 | |
| (509) LDFYNLWNTFTKLQ | SEQ ID NO: 10073 | |
| (508) FDFYNLWNTFTKLQ | SEQ ID NO: 10074 | |
| (508) FDFYNLWNTFTKLQ | SEQ ID NO: 10075 | |
| (507) FDFYNLWNTFTKLQ | SEQ ID NO: 10076 | |
| (511) FDFYNLWNTFTKLQ | SEQ ID NO: 10077 | |

FIGURE 119

tagtcaaaacccacagaatgattccagcaggcataagtatctgatgaagtagaaaagcaa
- - - V S D E V E K Q
gttgacacgt**TTG**tcacacagacaacacggttctttcaggtccaatc**TTG**acaaagtacttc
V A R L S H R Q H V L S G P I L T K Y F
attgatgtaagctcaaagccatgcgcccaaaggacgaacacgactctgtctgacaatcct
I D V S S K P C A Q R T N T T L S D N P
ttcagtgtatcactgagcatttgtactatcttaatacgcactacattccagggcaagcct
F S V S L S I C T I L I R T T F Q G K P
ttatac**ATG**agtgggtataagatgtttaactgctcactgggtggaggtttgtgcattaact
L Y M S G I R C L N C S L V E V C A L T
Ctgggtgaattttgtgttattttcagtgtcaacataa **SEQ ID NO: 10080**
L V N F V L F S V S T - **SEQ ID NO: 10027**

FIGURE 120**FIGURE 120A**

PRHTQRT-PTVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQ
LEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSNLILYH
SCIKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKER
VVCVTNVQLAFLHQLMPAGIILWVLTMSITHL-LMFSSGALRVTFRVMTNIA
RYMEMHMLVVMLS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTWL
-SLHCLLISFQFFMT-EIQRLSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILML
YITINSLMVFCFIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVCM-ISMHS
TLQLSIKVHLLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VV
LFADTMQMSTDSTWMHII--FLLDLAYGFTNNLILITCGIHLPGYRV

FIGURE 120B

LGIPKGHDLP-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN
-RCCGY-PTSPARIFYRC-LSSCTDWLC-H-K-HRIHQ-SCKTSTR-PV-TSYTT
HV-RLALECSAY-DSTNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNV
LSV-QTCNLLFYFIRYLCLLESFCGF-LCL-PIYD-CSAVGLYG-PSE-P-PTLP
GTWKCTCG-L-CYHD-MFSSP-VLC-AR-LVC-IPYYRR-TEG-FCLQKSTTHGC
EVCIA--VSSSS-HRKSKEYQVCASG-SRMEVLRCSAM--QSLQNRGTLLFLCY
TSR-IH-WCLFVLEL-R-SLPSQCNCV-V-HKSLVKLELTRL-WW-FVCE-ACIP
HSSFR-KCIY-FKAIAFLLLF--SL-VSWQTSSVGY-LCSTQICYVYYTMQFRWC
CLQTPCK-VPTVLGCI-YDDFCWI-PMDLQTI-YL-PVEYIYQVTEF

FIGURE 120C

-AYPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG
TNLPLQLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVV
RIKIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD
TYACWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAV
HECFVKRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCPV
QAEVEWKFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVD RY PANAI VCRFD
TRVLSN LNLP GCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS
IDYVPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNT
FTRLQSL

FIGURE 120D

-TL-PGKCIPQVISIKLFVNP-AKSSRNHHIICIQVLSVLICMVSANSTT-IASCNTRSR
FEWNIINIRHYLFAMRLTRTIRIVKERQLL-ISKCTFIESWSVECMLIHIQTTTITAW-V
QV-QDSCVKPTHNCIGWVTINVTIPKQNTISEFIVMYSIRIEEFLYFVSFVTTWLSIVE
LPFYFSLRHTLDSLWISYVMKNWKLI SKQ CRLHNVLYFSASRINPQFISYNRVFNRPIN
ALNKALMDC-TSSHDSITTSHMCISMYLAMLVMVTLKVTRKAPLLNINHKKWVIDIVKTHR
MIPAGISI--SRKASCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITE
HLYYLNTHYIPGQAFIHEWYKMFKLVTWWRFCINSGEFCVIFSVNITSRYSY-VNTPCRKS
-LER-VSTHSISSCMTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDESTVG
HVLWVCL

FIGURE 120E

KLCNLVN VFHRL-VSNCL-IHRLNPAEIIILYASKYCRYSAWCLQTAPPKLHRVIVHAD
LSGT-SISDTTCLP-DSQGLSE--KKGNCFKLVNALLSKAGVWNACLFYKLPSPQPGKF
KFDKTLVSNLHTIALAG-RSTLQFQNKQTPSVNLS-CIA-E-KSSSIL-ALSLHG-AS-N
FHSTSA-GTHLIAFGFPMS-RTGNLSASNADFTTMCCTFLQAELTLSSSPIIGYSTDQST
RLTKHSWTAKHLVMIASQLATCAFPCTWQCWSWLL-RLPVKPHC-TSIINGL-T-SKPTE
-FQQA-VSDEVEKQVARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTTSLDNPFVSLS
ICTILIRTTFQKPLYMSGIRCLNWSPGGGFALTLVNSVLF SVST-PVGTATKLT PVENP
SWRGRLVPTASLVA-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR-V
MSFGYA-

FIGURE 120F

NSVTW-MYSTGYKYQIVCKSIG-IQKSSYYMHPSTVGTHLHGVCQHHLNCIV-YT-QI
-VEHNQYPTLLVCHETHKDYQNSKRKAIALN--MHFYRKLECGMHAYSHTNYHHHSLVSS
SLTRLLCQTYTQLHWLGNDQRYNSKTNKHHQ-IYRDV-HKNRRVPLFCKLCHYMAEHRRT
SILLQPEAHT--PLDFLCHEELETYQQAMQTSQPCVVLFCCKQN-PSVHLL--GIQQTNR
A-QSTHGLLNI-S--HHN-PHVHFHVPGNVGHGYSEGYP-SPTAEHQ-S-MGYRHSQNPQN
DSSRHKYLK-KSKLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-A
FVLS-YALHSRASLYT-VV-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KIL
AGEVG-YPQHL-LHDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYGRS
CPLGMPR

FIGURE 121

| | | | | | | |
|-----------------|---|-----|-----|-----|-----|-----|
| | 10 | 20 | 30 | 40 | 50 | 60 |
| SEQ ID NO:10033 | -----TACCGTAGACTCATCTCTATGATGGGTTTCAAAA | | | | | |
| SEQ ID NO:10084 | CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA | | | | | |
| Consensus | TACCGTAGACTCATCTCTATGATGGGTTTCAAAA | | | | | |
| Prim. cons. | CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA | | | | | |
| | 70 | 80 | 90 | 100 | 110 | 120 |
| SEQ ID NO:10033 | TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC | | | | | |
| SEQ ID NO:10084 | TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC | | | | | |
| Consensus | TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC | | | | | |
| Prim. cons. | TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC | | | | | |
| | 130 | 140 | 150 | 160 | 170 | 180 |
| SEQ ID NO:10033 | ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG | | | | | |
| SEQ ID NO:10084 | ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG | | | | | |
| Consensus | ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG | | | | | |
| Prim. cons. | ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG | | | | | |
| | 190 | 200 | 210 | 220 | 230 | 240 |
| SEQ ID NO:10033 | GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA | | | | | |
| SEQ ID NO:10084 | GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA | | | | | |
| Consensus | GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA | | | | | |
| Prim. cons. | GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA | | | | | |
| | 250 | 260 | 270 | 280 | 290 | 300 |
| SEQ ID NO:10033 | CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC | | | | | |
| SEQ ID NO:10084 | CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC | | | | | |
| Consensus | CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC | | | | | |
| Prim. cons. | CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC | | | | | |
| | 310 | 320 | 330 | 340 | 350 | 360 |
| SEQ ID NO:10033 | CAGGTGACCAGTTTAAACATCTTATACC----- | | | | | |
| SEQ ID NO:10084 | CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG | | | | | |
| Consensus | CAGGTGACCAGTTTAAACATCTTATACC | | | | | |
| Prim. cons. | CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG | | | | | |

etc.

FIGURE 122**5'3' Frame 1**

cctagggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaa
P R H T Q R T - P T V D S S L - W V S K
tgaattaccaagtcaatgggttaccctaatatgtttatcacccgcgaagaagctattcgtc
- I T K S M V T L I C L S P A K K L F V
acgttcgtgctggattggcctttgatgtagagggctgtcatgcaactagagatgctgtgg
T F V R G L A L M - R A V M Q L E M L W
gtactaacctacctctccagctaggattttctacaggtgttaacttagtagctgtaccga
V L T Y L S S - D F L Q V L T - - L Y R
ctggttatgttgacactgaaaataacacagaattcaccagaggttaatgcaaacctccac
L V M L T L K I T Q N S P E L M Q N L H
caggtgaccagtttaaacatcttataccactcatgtataaaggcttgccctggaatgtag
Q V T S L N I L Y H S C I K A C P G M -
tgcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcg
C V L R - Y K C S V I H - K D C Q T E S
tgttcgtcctttgggcgcgtggcctttgagcttacatcaatgaagtactttgtcaagattg
C S S F G R M A L S L H Q - S T L S R L
gacctgaaagaacgtgttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcag
D L K E R V V C V T N V Q L A F L L H Q
atacttatgcctgctggaatcattctgtgggttttgactatgtctataaccctttatga
I L M P A G I I L W V L T M S I T H L -
ttgatgttcagcagtggggctttacgggtaaccttcagagtaaccatgaccaacattgcc
L M F S S G A L R V T F R V T M T N I A
aggtacatggaaatgcacatgtggctagtgtgatgctatcatgactagatgttttagcag
R Y M E M H M W L V V M L S - L D V - Q
tccatgagtgctttgttaagcgcgttgattgggtctgttgaataccctattataggagatg
S M S A L L S A L I G L L N T L L - E M
aactgaggggttaattctgcttgcaaaaagtacaacacatggttgtgaagtctgcattgc
N - G L I L L A E K Y N T W L - S L H C
ttgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgc
L L I S F Q F F M T - E I Q R L S S V C
ctcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaca
L R L K - N G S S T M L S H V V T K L T
aaatagaggaactcttctatttcttatgctatacatcacgataaattcactgatgggtgttt
K - R N S S I L M L Y I T I N S L M V F
gtttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttg
V C F G I V T L I V T Q P M Q L C V G L
acacaagagtcttgtcaaacttgaacttaccaggctgtgatgggtggtagtttgtatgtga
T Q E S C Q T - T Y Q A V M V V V C M -
ataagcatgcattccacactccagcttttcgataaaaagtgcatttactaatttaaagcaat
I S M H S T L Q L S I K V H L L I - S N
tgccctttcttttactatttctgatagtccttgtgagtcctcatggcaaacaagtagtgctcg
C L S F T I L I V L V S L M A N K - C R
atattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtg
I L I M F H S N L L R V L H D A I - V V
ctgtttgcagacaccatgcaaatgagtaccgacagtacttggtatgcatataatatgatga
L F A D T M Q M S T D S T W M H I I - -
tttctgctggatttagcctatggatttacaacaatttgatacttataacctgtggaata
F L L D L A Y G F T N N L I L I T C G I

catttaccaggttacagagttta
H L P G Y R V

5'3' Frame 2

cctagggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaat
L G I P K G H D L P - T H L Y D G F Q N
gaattaccaagtcaatgggtaccctaatatgtttatcacccgcgaagaagctattcgtca
E L P S Q W L P - Y V Y H P R R S Y S S
cgttcgtgcggtggattggcctttgatgtagagggctgtcatgcaactagagatgctgtggg
R S C V D W L - C R G L S C N - R C C G
tactaacctacctctccagctaggatctttctacaggtgttaacttagtagctgtaccgac
Y - P T S P A R I F Y R C - L S S C T D
tgggttatgttgacactgaaaataacacagaattcaccagagttaatgcaaaacctccacc
W L C - H - K - H R I H Q S - C K T S T
aggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtagt
R - P V - T S Y T T H V - R L A L E C S
gcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgt
A Y - D S T N A Q - Y T E R I V R Q S R
gttcgtcctttgggcgcatggcctttgagcttacatcaatgaagtactttgtcaagattgg
V R P L G A W L - A Y I N E V L C Q D W
acctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcaga
T - K N V L S V - Q T C N L L F Y F I R
tacttatgcctgctggaatcattctgtggggttttgactatgtctataacccatttatgat
Y L C L L E S F C G F - L C L - P I Y D
tgatgttcagcagtggggcttttacgggtaaccttcagagtaacctatgaccaacattgcca
- C S A V G L Y G - P S E - P - P T L P
ggtacatggaaatgcacatgtggctagttgtgatgctatcatgactagatgttttagcagt
G T W K C T C G - L - C Y H D - M F S S
ccatgagtgctttgttaagcgcgttgattgggtctgttggaataccctattataggagatga
P - V L C - A R - L V C - I P Y Y R R -
actgagggttaattctgcttgcagaaaagtacaacacatgggtgtgaagtcgtcattgct
T E G - F C L Q K S T T H G C E V C I A
tgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgcc
C - - V S S S S - H R K S K G Y Q V C A
tcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaciaa
S G - S R M E V L R C S A M - - Q S L Q
aatagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgtttg
N R G T L L F L C Y T S R - I H - W C L
tttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttga
F V L E L - R - S L P S Q C N C V - V -
cacaagagtcttgtcaaacttgaacttaccaggctgtgatgggtgtagtttgtatgtgaa
H K S L V K L E L T R L - W W - F V C E
taagcatgcattccacactccagcttttcgataaaagtgcatttactaatttaaagcaatt
- A C I P H S S F R - K C I Y - F K A I
gcctttcttttactattctgatagtccttgtgagtcctcatggcaaacaagtagtgctcgga
A F L L L F - - S L - V S W Q T S S V G
tattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtgc
Y - L C S T Q I C Y V Y Y T M Q F R W C
tgtttgcagacaccatgcaaatgagtaccgacagtagtcttggtatgcataatatgatgat

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C L Q T P C K - V P T V L G C I - Y D D
 ttctgctggatttagcctatggattttacaaacaatttgatacttataacctgtggaatac
 F C W I - P M D L Q T I - Y L - P V E Y
 atttaccagggttacagagttta
 I Y Q V T E F

5'3' Frame 3

cctaggcatacccaaaggacATGacctaccgtagactcatctctatgatggggtttcaaaatg
 - A Y P K D M T Y R R L I S M M G F K M
 aattaccaagtcaatgggttacctaataatgtttatcacccgcgaagaagctattcgtcac
 N Y Q V N G Y P N M F I T R E E A I R H
 gttcgtgctggattgggtttgatgtagagggctgtcatgcaactagagatgctgtgggt
 V R A W I G F D V E G C H A T R D A V G
 actaacctacctctccagctaggattttctacaggtgttaacttagtagctgtaccgact
 T N L P L Q L G F S T G V N L V A V P T
 gggtatgttgacactgaaaataacacagaattcaccagagttaatgcaaaccctccacca
 G Y V D T E N N T E F T R V N A K P P P
 ggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccttggaatgtagtg
 G D Q F K H L I P L M Y K G L P W N V V
 cgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgtg
 R I K I V Q M L S D T L K G L S D R V V
 ttcgtcctttgggcgcattgggtttgagcttacatcaatgaagtactttgtcaagattgga
 F V L W A H G F E L T S M K Y F V K I G
 cctgaaagaacgtgttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcagat
 P E R T C C L C D K R A T C F S T S S D
 acttatgcctgctggaatcattctgtgggttttgactatgtctataaccatttatgatt
 T Y A C W N H S V G F D Y V Y N P F M I
 gatgttcagcagtggggttttacgggttaaccttcagagtaaccatgaccaacattgccag
 D V Q Q W G F T G N L Q S N H D Q H C Q
 gtacatggaaatgcacatgtggctagtgtgatgctatcatgactagatgttttagcagtc
 V H G N A H V A S C D A I M T R C L A V
 catgagtgctttgttaagcgcgttgattgggtctgttgataaccctattataggagatgaa
 H E C F V K R V D W S V E Y P I I G D E
 ctgaggggttaattctgcttgcagaaaagtacaacacatgggttggaagtctgcattgctt
 L R V N S A C R K V Q H M V V K S A L L
 gctgataagtttccagtttcttcatgacataggaaatccaaaggctatcaagtgtgtgcct
 A D K F P V L H D I G N P K A I K C V P
 caggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttacaaa
 Q A E V E W K F Y D A Q P C S D K A Y K
 atagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgtttgt
 I E E L F Y S Y A I H H D K F T D G V C
 ttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgttaggtttgac
 L F W N C N V D R Y P A N A I V C R F D
 acaagagtcttgtcaaaccttgaacttaccagggtgtgatgggtgtagttttgtatgtgaat
 T R V L S N L N L P G C D G G S L Y V N
 aagcatgcattccacactccagcttttcgataaaaagtgcatttactaatttaaagcaattg
 K H A F H T P A F D K S A F T N L K Q L
 ccttttcttttactattctgatagtccttgtgagtcctcatggcaaacaagtagtgctcgat
 P F F Y Y S D S P C E S H G K Q V V S D

attgattatgttccactcaaatctgctacgtgtattacacgatgcaatttaggtggtgct
I D Y V P L K S A T C I T R C N L G G A
gtttgcagacacccatgcaaatgagtaccgacagtacttggatgcatataatatgatgatt
V C R H H A N E Y R Q Y L D A Y N M M I
tctgctggatttagcctatggatttacaaacaatttgatacttataacctgtggaataca
S A G F S L W I Y K Q F D T Y N L W N T
tttaccaggttacagagttta
F T R L Q S L

3'5' Frame 1

taaactctgtaacctggtaaattgtattccacagggttataagtatcaaattgtttgtaaatt
- T L - P G K C I P Q V I S I K L F V N
ccataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcgggtactc
P - A K S S R N H H I I C I Q V L S V L
atttgcatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcaga
I C M V S A N S T T - I A S C N T R S R
tttgagtgggaacataatcaatatccgacactacttgtttgccatgagactcacaaggact
F E W N I I N I R H Y L F A M R L T R T
atcagaatagtaaaaagaaaggcaattgcttttaaattagtaaatgcacttttatcgaaagc
I R I V K E R Q L L - I S K C T F I E S
tggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagtt
W S V E C M L I H I Q T T T I T A W - V
caagtttgacaagactcttgtgtcaaacctacacacaattgcattgggctgggtaacgatc
Q V - Q D S C V K P T H N C I G W V T I
aacgtttacaattccaaaacaaacaaacaccatcagtgaatttatcgtgatgtatagcata
N V T I P K Q T N T I S E F I V M Y S I
agaatagaagagttcctctattttgtaagctttgtcactacatgggtgagcatcgtagaa
R I E E F L Y F V S F V T T W L S I V E
cttccattctacttcagcctgaggcacacacttgatagcctttggatttcctatgtcatg
L P F Y F S L R H T L D S L W I S Y V M
aagaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttggtacttttct
K N W K L I S K Q C R L H N H V L Y F S
gcaagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaac
A S R I N P Q F I S Y N R V F N R P I N
gcgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacaaactagc
A L N K A L M D C - T S S H D S I T T S
cacatgtgcatttccatgtacctggcaatgttggtcatgggttactctgaaggttaccggt
H M C I S M Y L A M L V M V T L K V T R
aaagccccactgctgaacatcaatcataaatgggttatagacatagtcaaaaccacaga
K A P L L N I N H K W V I D I V K T H R
atgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcaca
M I P A G I S I - - S R K A S C T F V T
cagacaacacgttcttttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaa
Q T T R S F R S N L D K V L H - C K L K
gccatgcgccccaaaggacgaacacgactctgtctgacaatcctttcagtgatatcactgag
A M R P K D E H D S V - Q S F Q C I T E
catttggtactatcttaatacgcactacattccaggggcaagcctttatacatgagtggtat
H L Y Y L N T H Y I P G Q A F I H E W Y
aagatgttttaaactgggtcacctgggtggagggttttgcattaactctgggtgaattctgtgtt

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K M F K L V T W W R F C I N S G E F C V
attttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcc
I F S V N I T S R Y S Y - V N T C R K S
tagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatc
- L E R - V S T H S I S S C M T A L Y I
aaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagg
K A N P R T N V T N S F F A G D K H I R
gtaaccattgacttggttaattcattttgaaacccatcatagagatgagtgtaggttaggt
V T I D L V I H F E T H H R D E S T V G
catgtccttttgggtatgcctagg
H V L W V C L

3'5' Frame 2

taaactctgtaacctggtaaatgtattccacaggttataagtatcaaattgtttgtaaattc
K L C N L V N V F H R L - V S N C L - I
cataggctaaatccagcagaaatcatcatatttatatgcatccaagtactgtcgggtactca
H R L N P A E I I I L Y A S K Y C R Y S
tttgcattggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagat
F A W C L Q T A P P K L H R V I H V A D
ttgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggacta
L S G T - S I S D T T C L P - D S Q G L
tcagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcacttttatcgaaagct
S E - - K K G N C F K L V N A L L S K A
ggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttc
G V W N A C L F T Y K L P P S Q P G K F
aagtttgacaagactccttggtgtcaaacctacacacaattgcattgggtgggtaacgatca
K F D K T L V S N L H T I A L A G - R S
acgttacaattccaaaacaaacaaacaccatcagtgatttatcgtgatgtatagcataa
T L Q F Q N K Q T P S V N L S - C I A -
gaatagaagagttcctctattttgtaagctttgtcactacatggctgagcatcgtagaac
E - K S S S I L - A L S L H G - A S - N
ttccattctacttcagcctgaggcacacacttgatagccttttgatttcctatgtcatga
F H S T S A - G T H L I A F G F P M S -
agaactggaaacttatcagcaagcaatgcagacttcacaacccatgtgttgacttttctg
R T G N L S A S N A D F T T M C C T F L
caagcagaattaaccctcagttcatctcctataataggggtattcaacagaccaatcaacg
Q A E L T L S S S P I I G Y S T D Q S T
cgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacaactagcc
R L T K H S W T A K H L V M I A S Q L A
acatgtgcattttccatgtacctggcaatgttggtcatgggttactctgaagggttaccgta
T C A F P C T W Q C W S W L L - R L P V
aagccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaa
K P H C - T S I I N G L - T - S K P T E
tgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacac
- F Q Q A - V S D E V E K Q V A R L S H
agacaacacgttcttttcaggtccaatcttgacaaagttacttcattgatgtaagctcaaag
R Q H V L S G P I L T K Y F I D V S S K
ccatgcgccccaaaggacgaacacgactctgtctgacaatccttttcagtgatcactgagc
P C A Q R T N T T L S D N P F S V S L S

at ttgtactatcttaatacgcactacattccagggcaagcctttatacatgagtgggtata
I C T I L I R T T F Q G K P L Y M S G I
agatgttttaactggtcacctgggtggaggtttttgcattaactctgggtgaattctgtgtta
R C L N W S P G G G F A L T L V N S V L
ttttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcct
F S V S T - P V G T A T K L T P V E N P
agctggagaggttaggttagtaccacacagcatctcttagttgcatgacagccctctacatca
S W R G R L V P T A S L V A - Q P S T S
aagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattaggg
K P I H A R T - R I A S S R V I N I L G
taaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggtaggtc
- P L T W - F I L K P I I E M S L R - V
atgtcctttgggtatgcctagg
M S F G Y A -

3'5' Frame 3

taaactctgtaacctggtaaatgtattccacaggttataagtatcaaattgtttgtaaattcc
N S V T W - M Y S T G Y K Y Q I V C K S
ataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcgggtactcat
I G - I Q Q K S S Y Y M H P S T V G T H
ttgcatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagatt
L H G V C K Q H H L N C I V - Y T - Q I
tgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggactat
- V E H N Q Y P T L L V C H E T H K D Y
cagaatagtaaaaagaaaggcaattgcttttaaattagtaaatgcactttttatcgaaagctg
Q N S K R K A I A L N - - M H F Y R K L
gagtggtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttca
E C G M H A Y S H T N Y H H H S L V S S
agtttgacaagactccttggtgtcaaacctacacacaattgcattgggtgggtaacgatcaa
S L T R L L C Q T Y T Q L H W L G N D Q
cgttacaattccaaaacaaaacaccatcagtggaatttatcgtgatgtatagcataag
R Y N S K T N K H H Q - I Y R D V - H K
aatagaagagttcctctattttgtaagctttgtcactacatgggtgagcatcgtagaact
N R R V P L F C K L C H Y M A E H R R T
tccattctacttcagcctgaggcacacacttgatagcctttggatttcctatgtcatgaa
S I L L Q P E A H T - - P L D F L C H E
gaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgtttgtacttttctgc
E L E T Y Q Q A M Q T S Q P C V V L F C
aagcagaattaaccctcagttcatctcctataataggggtattcaacagaccaatcaacgc
K Q N - P S V H L L - - G I Q Q T N Q R
gcttaacaaagcactcatggactgctaacaatctagtcatgatagcatcacaactagcca
A - Q S T H G L L N I - S - - H H N - P
catgtgcattttccatgtacctggcaatgttggtcatggttactctgaagggttaccctgtaa
H V H F H V P G N V G H G Y S E G Y P -
agccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaat
S P T A E H Q S - M G Y R H S Q N P Q N
gattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacaca
D S S R H K Y L M K - K S K L H V C H T
gacaacacgttctttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaagc

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D N T F F Q V Q S - Q S T S L M - A Q S
catgcgccccaaaggacgaacacgactctgtctgacaatcctttcagtgtatcactgagca
H A P K G R T R L C L T I L S V Y H - A
tttgtactatcttaatacgcactacattccaggggcaagcctttatacatgagtggtataa
F V L S - Y A L H S R A S L Y T - V V -
gatgttttaaactgggtcacctgggtggagggttttgcattaactctgggtgaattctgtgttat
D V - T G H L V E V L H - L W - I L C Y
tttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatccta
F Q C Q H N Q S V Q L L S - H L - K I L
gctggagaggttaggttagtacccacagcatctctagttgcatgacagccctctacatcaa
A G E V G - Y P Q H L - L H D S P L H Q
agccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagggt
S Q S T H E R D E - L L R G - - T Y - G
aaccattgacttggtaattcatttttgaaacccatcatagagatgagtctacggtaggtca
N H - L G N S F - N P S - R - V Y G R S
tgtcctttgggtatgcctagg
C P L G M P R

FIGURE 123

CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGT
.....i.....N..N.....i.....N....
TACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTACCGTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCA
.....i.....N.....N
TGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
.....N.....
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACAT
.....N.....N.....
CTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCCTATTAAGATAGTACAAATGCTCAGTGATACACTGAA
.....N.....N.....N.....
AGGATTGTCAGACAGAGTCGTGTTTCGTCTTTGGGCGCATGGCTTTGAGCTTACATCAATGAAGTACTTTGTCAAGATTG
.....N.....N.....
GACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAAT
.....N.....
CATTCTGTGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAG
.....N.....N.....N.....
TAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAG
.....N.....N.....N.....N.....i.....N.....
TCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAATACCTATTATAGGAGATGAAC TGAGGGTTAATTCTGCT
..N.....N.....
TGCAGAAAAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCCTTCATGACATAGGAAATCC
.....i.....N.....
AAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTTACA
.....N.....N.....N.....
AAATAGAGGAACTCTTCTATTCTTATGCTATAACATCACGATAAATTCAGTATGGTGTGTTTGTGTTTGGGAATTGTAAC
.....N.....N.....
GTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACCTTGAACCTACCAGGCTGTGA
.....N.....N.....
TGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAAT
.....N.....N.....
TGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATGGCAAACAAGTAGTGTCCGATATTGATTATGTTCCACTC
.....i.....N.....
AAATCTGCTACGTGTATTACACGATGCAATTTAGGTGGTGTGTTTGCAGACACCATGCAATGAGTACCGACAGTACTT
.....N.....N.....N.....
GGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATA
..N.....N..N.....N.....
CATTTACCAGGTTACAGAGTTTA **SEQ ID NO: 10084**
.....

FIGURE 123 (contd.)

| Pos | Score | Pred |
|------|-------|------|
| 21 | 0.651 | Yes |
| 45 | 0.354 | - |
| 48 | 0.387 | - |
| 60 | 0.590 | Yes |
| 76 | 0.470 | - |
| 90 | 0.676 | Yes |
| 145 | 0.192 | - |
| 160 | 0.410 | - |
| 172 | 0.290 | - |
| 247 | 0.221 | - |
| 286 | 0.219 | - |
| 333 | 0.373 | - |
| 355 | 0.178 | - |
| 381 | 0.286 | - |
| 439 | 0.405 | - |
| 459 | 0.204 | - |
| 547 | 0.289 | - |
| 580 | 0.447 | - |
| 597 | 0.449 | - |
| 604 | 0.290 | - |
| 646 | 0.427 | - |
| 667 | 0.427 | - |
| 673 | 0.208 | - |
| 679 | 0.317 | - |
| 694 | 0.180 | - |
| 702 | 0.554 | Yes |
| 710 | 0.151 | - |
| 724 | 0.384 | - |
| 778 | 0.151 | - |
| 819 | 0.711 | Yes |
| 865 | 0.306 | - |
| 917 | 0.230 | - |
| 931 | 0.214 | - |
| 941 | 0.190 | - |
| 985 | 0.274 | - |
| 1012 | 0.368 | - |
| 1060 | 0.206 | - |
| 1120 | 0.193 | - |
| 1135 | 0.185 | - |
| 1147 | 0.431 | - |
| 1240 | 0.562 | Yes |
| 1270 | 0.377 | - |
| 1304 | 0.190 | - |
| 1336 | 0.353 | - |
| 1342 | 0.312 | - |
| 1363 | 0.213 | - |
| 1374 | 0.178 | - |
| 1377 | 0.096 | - |
| 1400 | 0.056 | - |

FIGURE 124

| Sequences: | | | | (bits) | Value |
|------------|----------|-----------------|--|--------|-------|
| gi | 74827 | pir | VFIHJH genome polyprotein 1b - murine hepatit... | 638 | 0.0 |
| gi | 14917044 | sp P29982 | RRPB_CVMJH RNA-directed RNA polymeras... | 637 | 0.0 |
| gi | 26007546 | ref NP_068668.2 | ORF1ab polyprotein [Murine hep... | 637 | 0.0 |
| gi | 7769342 | gb AAF69332.1 | AF208066_2 RNA-directed RNA polyme... | 637 | 0.0 |
| gi | 6625761 | gb AAF19384.1 | AF201929_2 RNA-directed RNA polyme... | 637 | 0.0 |
| gi | 2641128 | gb AAB86818.1 | RNA-directed RNA polymerase [muri... | 635 | 0.0 |
| gi | 4377413 | emb CAA36202.1 | open reading frame 1b (AA 1-2733... | 634 | 0.0 |
| gi | 133592 | sp P16342 | RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE ... | 634 | 0.0 |
| gi | 26008080 | ref NP_150073.2 | orflab polyprotein [Bovine cor... | 633 | e-180 |
| gi | 15077820 | gb AAK83365.1 | replicase [bovine coronavirus] | 633 | e-180 |
| gi | 18033972 | gb AAL57305.1 | replicase [bovine coronavirus] | 633 | e-180 |
| gi | 7769353 | gb AAF69342.1 | AF208067_2 RNA-directed RNA polyme... | 633 | e-180 |
| gi | 17529672 | gb AAL40397.1 | AF220295_2 RNA polymerase 1b [bov... | 623 | e-177 |
| gi | 25121571 | ref NP_740618.1 | coronavirus nsp11 [Murine hepa... | 622 | e-177 |
| gi | 26008092 | ref NP_742140.1 | coronavirus nsp11 [Bovine coro... | 617 | e-175 |
| gi | 10242469 | ref NP_066134.1 | ORF1ab polyprotein; frameshift... | 575 | e-163 |
| gi | 14149033 | emb CAC39112.1 | replicase polyprotein 1ab [Avia... | 575 | e-163 |
| gi | 458735 | emb CAA83018.1 | potential chimeric protein [Avian... | 570 | e-161 |
| gi | 133594 | sp P26314 | RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (...) | 570 | e-161 |
| gi | 29293454 | gb AAO67706.1 | ORF1b polyprotein [Avian infecti... | 565 | e-160 |
| gi | 25121555 | ref NP_740631.1 | coronavirus nsp11 [Avian infec... | 559 | e-158 |
| gi | 9635157 | ref NP_058422.1 | replicase [Transmissible gastro... | 545 | e-153 |
| gi | 19387582 | ref NP_598309.1 | Pol1 [porcine epidemic diarrhe... | 541 | e-152 |
| gi | 12175747 | ref NP_073549.1 | replicase polyprotein 1ab [Hum... | 535 | e-151 |
| gi | 133591 | sp P18458 | RRPB_BEV RNA-directed RNA polymerase (O... | 50 | 8e-05 |
| gi | 1513061 | dbj BAA13323.1 | cyanoprotein alpha subunit precu... | 35 | 3.7 |

Alignments

>gi|74827|pir|VFIHJH genome polyprotein 1b - murine hepatitis virus
(strain JHM)

Length = 2731

Score = 638 bits (1645), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGNTNLPQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHATRDSIGTNFPLQ 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRKIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCSVCNKRATCFNSRTGYGWCWR 1764

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1765 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1824

157/193

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAICVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVND+YPANA+VCRFDTRVLS
Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLSK 1939

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 1940 LNLPGCNGGSLYVNKHAFHTNPFTRAFAFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2059

Query: 486 L 486
L
Sbjct: 2060 L 2060

>gi|14917044|sp|P29982|RRPB_CVMJH RNA-directed RNA polymerase (ORF1B)
gi|7583321|gb|AAA46458.2| open reading frame 1b [murine hepatitis virus]
Length = 2731

Score = 637 bits (1644), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 1585 VTYSRLISLMGFKLDLTLDDGYCKLFITRDEAIKRVRAWVGFDAGAHATRDSIGTNFPLQ 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLVPLMSRQKQWDVVRIRIVQ 1704

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVCSVCNKRATCFNSRTGYGWCWR 1764

Query: 186 HSVGFDYVYNPFMIDVQWQGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QWQW+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
Sbjct: 1765 HSYSCDYLYNPLIVDIQWQGTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAICVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVND+YPANA+VCRFDTRVLS
Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLSK 1939

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 1940 LNLPGCNGGSLYVNKHAFHTNPFTRAFAFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 1999

158/193

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2059

Query: 486 L 486
L
Sbjct: 2060 L 2060

>gi|26007546|ref|NP_068668.2| ORFlab polyprotein [Murine hepatitis virus]
Length = 7178

Score = 637 bits (1644), Expect = 0.0
Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
Sbjct: 6032 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAIRDSIGTNFPLQ 6091

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
Sbjct: 6092 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 6151

Query: 126 MLSDTLKGLSDRVVFLWAHGFEITSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
Sbjct: 6152 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYYGCWR 6211

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
Sbjct: 6212 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 6271

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 6272 SVNWNLEYPIISNEVSVNTSRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 6329

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+
Sbjct: 6330 KFYDASPV---VKS VKQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 6386

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVPL 425
LNLPGC+GGSLYVnKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 6387 LNLPGCNGGSlyVnKHAFHTSPFTRAAFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 6446

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 6447 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 6506

Query: 486 L 486
L
Sbjct: 6507 L 6507

>gi|7769342|gb|AAF69332.1|AF208066_2 RNA-directed RNA polymerase [murine
hepatitis virus]
Length = 2732

Score = 637 bits (1644), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 1586 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ 1645

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
Sbjct: 1646 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIVQ 1705

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
Sbjct: 1706 MLSDDLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVKNRATCFNSRTGYYGCWR 1765

Query: 186 HSVGFDYVYNPFMIDVQWGF'TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QWQG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
Sbjct: 1766 HSYSCDYLYNPLIVDIQWGYTGSLTSNHDLCVHKGAVHASSDAIMTRCLAVHDCFCCK 1825

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 1826 SVNWSLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1883

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+
Sbjct: 1884 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1940

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 1941 LNLPGCNGGSLYVNKHAFHTSPFTRAFAENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2000

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 2001 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2060

Query: 486 L 486
L
Sbjct: 2061 L 2061

>gi|6625761|gb|AAF19384.1|AF201929_2 RNA-directed RNA polymerase [murine hepatitis virus strain 2]

gi|7739595|gb|AAF68920.1|AF207902_2 RNA-directed RNA polymerase [murine hepatitis virus strain ML-11]

Length = 2733

Score = 637 bits (1643), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

160/193

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVCKNRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTNSHDLICSVHKGAVHASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWSLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRAFFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486
L

Sbjct: 2062 L 2062

>gi|2641128|gb|AAB86818.1| RNA-directed RNA polymerase [murine hepatitis virus]

Length = 2733

Score = 635 bits (1637), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTNSHDPICSVHKGAVHASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

161/193

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMKQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486
 L

Sbjct: 2062 L 2062

>gi|4377413|emb|CAA36202.1| open reading frame 1b (AA 1-2733) [Murine hepatitis virus]
 Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMKQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

162/193

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486

L

Sbjct: 2062 L 2062

>gi|133592|sp|P16342|RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE (ORF1B)
gi|93916|pir|S15760 genome polyprotein - murine hepatitis virus (strain
A59)

Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65

+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125

LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185

MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVCVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245

HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVHASSDAIMTRCLAVHDCFCK 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAICVPQAEVEW 305

V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365

KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKS VKQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425

LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485

+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486

L

Sbjct: 2062 L 2062

>gi|26008080|ref|NP_150073.2| orflab polyprotein [Bovine coronavirus]

Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAEGAHATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGGYGCWR 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVND+YP NA+VCRFDTRVL+N
 Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVNDKYPPNAVVCRFDTRVLNN 6302

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 6303 LNLPGCNGGSLYVNKHAFHTKPFSSRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWYKTFDFYNLWNTFTKLQS 6422

Query: 486 L 486
 L
 Sbjct: 6423 L 6423

>gi|15077820|gb|AAK83365.1| replicase [bovine coronavirus]
 Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAEGAHATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGGYGCWR 6127

164/193

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMOVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N
Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAVVCRFDRVLNN 6302

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
Sbjct: 6303 LNLPGCNGGSLYVNKHAFHTKPF SRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS 6422

Query: 486 L 486
L
Sbjct: 6423 L 6423

>gi|18033972|gb|AAL57305.1| replicase [bovine coronavirus]
Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEA VKRVRAWVGFDAEGAHATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQ 125
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYYGCWR 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMOVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N
Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAVVCRFDRVLNN 6302

165/193

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDyVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 6303 LNLPGCNGGSlyVnKHAFHTKPFsRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDyVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDtYNLWNTfTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTfT+LQS
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTfTKLQS 6422

Query: 486 L 486
 L
 Sbjct: 6423 L 6423

>gi|7769353|gb|AAF69342.1|AF208067_2 RNA-directed RNA polymerase [murine hepatitis virus]
 Length = 2733

Score = 633 bits (1633), Expect = e-180

Identities = 285/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRawIGFDVEGCHATrDAVGtNLPLQ 65
 ++Y RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 1587 VSYRLISLMGFKLdLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGtNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENntEFTRVNAKPPPGDQFKHLIPLMYKGLPWNvVRIKIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGfELTSMKYfVKIGPERTCCLCDKRATCFSTSSDtyACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 1707 MLSdHLVdLADSVVLVTWAASFELTCLRYfAKVGREvVCSVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGaHVASSDAIMTRCLAVHdCFCK 1826

Query: 246 RVDWSVEYPIIGDELrvNSACrkVQhMVVKSALLADKFPVLHDIGNPKAIKCVpQAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1827 SVNWNLEYPiISNEVSVNTScRLlQRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELfYSYAIHhDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 1885 KFYDASPv---VKSvKQfVYKYEAHKDQFLDGLCMFWNCNVdKYPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDyVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1942 LNLPGCNGGSlyVnKHAFHTSPFTRAAFENLKPMPPFFYYSDTPCVYMEGMESKQVDyVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDtYNLWNTfTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTfT+LQS
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTfTRLQS 2061

Query: 486 L 486
 L
 Sbjct: 2062 L 2062

166/193

>gi|17529672|gb|AAL40397.1|AF220295_2 RNA polymerase 1b [bovine coronavirus]

Length = 2685

Score = 623 bits (1607), Expect = e-177

Identities = 282/481 (58%), Positives = 365/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1574 VTYSRLISLMGFKLDVTLG DYCKLFITKEEAVKRVRAWVGFD AEGAHATRDSIGTNFPLQ 1633

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 1634 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 1693

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C + KRAT +++ + Y CW
 Sbjct: 1694 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVSTKRATAYNSRTGYGWCWR 1753

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 1754 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 1813

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVK SALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 1814 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 1871

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDAQP ++ L Y + H D F DG+C+FWNCNV D+Y P NA+VCRFDTRVL+N
 Sbjct: 1872 KFYDAQPI---VKSVKTLLEYFFEAHKDSFKDGLCMFWNCNV DKYPPNAVVCRFDTRVLNN 1928

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425
 LNLPGC+GGS LYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 1929 LNLPGCNGGS LYVNKHAFHTKPF SRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 1988

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
 Sbjct: 1989 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS 2048

Query: 486 L 486
 L
 Sbjct: 2049 L 2049

>gi|25121571|ref|NP_740618.1| coronavirus nsp11 [Murine hepatitis virus]
 Length = 521

Score = 622 bits (1603), Expect = e-177

Identities = 284/479 (59%), Positives = 362/479 (75%), Gaps = 5/479 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 48 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAI RDSIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125

167/193

LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 108 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 167
 Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 168 MLSDDLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR 227
 Query: 186 HSVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 228 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 287
 Query: 246 RVDWSVEYPIIGDELVRNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 288 SVNWNLEYPIISNEVSVNTSCRLLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 345
 Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 346 KFYDASPV---VKS VKQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK 402
 Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 403 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL 462
 Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQ
 Sbjct: 463 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQ 521

>gi|26008092|ref|NP_742140.1| coronavirus nsp11 [Bovine coronavirus]
 Length = 521

Score = 617 bits (1590), Expect = e-175

Identities = 282/479 (58%), Positives = 365/479 (76%), Gaps = 5/479 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 48 VTYSRLISLMGFKLDVTLTDGYCKLFTITKEEAVKRVRAWVGFDAEGA HATRDSIGTNFPLQ 107
 Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 108 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 167
 Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 168 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGGYGCWR 227
 Query: 186 HSVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 228 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 287
 Query: 246 RVDWSVEYPIIGDELVRNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 288 NINWNVEYPIISNELSINTSCRVLQRMVLAAMLCNRYTLCDYDIGNPKAIACV--KDFDF 345
 Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

168/193

Sbjct: 346 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPPNAVVCRFDTRVLNN 402

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425
LNLPGC+GGS LYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 403 LNLPGCNGGS LYVNKHAFHTKPF SRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQ

Sbjct: 463 KSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQ 521

>gi|10242469|ref|NP_066134.1| ORFlab polyprotein; frameshift product [Avian
infectious bronchitis
virus]
Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG TNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP

Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIG TNLPL 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNV VRIKIV 124
Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV

Sbjct: 5575 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 5634

Query: 125 QMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD TYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 5635 QMLADNLCNVSDCVFVVTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGF TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F

Sbjct: 5694 KHCLGFDFVYNPLLVDIQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 5753

Query: 245 KRVDWSVEYPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMYL NACVDALKVNVVYDIGNPKGIKCVRRGDVN 5813

Query: 305 WKFYDAQPCSDKAYKIEELFY SYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNV D YP N++VCR+DTR LS

Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS 5870

Query: 365 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYV 424
NLPGC+GGS LYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 5871 VFNLPGCNGGS LYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAV TAGFTFWVTNKLNPYNLWKSFSALQ 5989

Query: 485 SL 486
S+

Sbjct: 5990 SI 5991

169/193

>gi|14149033|emb|CAC39112.1| replicase polyprotein lab [Avian infectious
bronchitis virus (strain
Beaudette CK)]
Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPLF 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 5575 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
QML+D L +SD VVFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
Sbjct: 5635 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSTQAYACW 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DAIMTRCLA++ F
Sbjct: 5694 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKYQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLNACVDALKVNVVYDIGNPKGIKCVRRGDVN 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNV D YP N++VCR+DTR LS
Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 5870

Query: 365 NLNLPGCDGGSlyVnkhafHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVP 424
NLPGC+GGSlyVnkhaf+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 5871 VFNLPGCNGGSlyVnkhafYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 5989

Query: 485 SL 486
S+
Sbjct: 5990 SI 5991

>gi|458735|emb|CAA83018.1| potential chimeric protein [Avian infectious
bronchitis virus]
Length = 2155

Score = 570 bits (1470), Expect = e-161

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 1596 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPLF 1655

170/193

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1656 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 1715

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 1716 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1774

Query: 185 NHSVGFVDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DAIMTRCLA++ F
 Sbjct: 1775 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 1834

Query: 245 KRVDWSVEYPIIGDELVRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 1835 QDVNWDLTYPHIANEDEVNSSCRYLQRMVYNACVDALKVNVVDIGNPKGIKCVRRGDVN 1894

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
 Sbjct: 1895 FRFYDKNPIVRNVKQFE--YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS 1951

Query: 365 NLNLPGLCDGGSGLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVP 424
 NLPGL+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 1952 VFNLPGLCNGGSGLYVNKHAFYTPKFDRIISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 2010

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
 Sbjct: 2011 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 2070

Query: 485 SL 486
 S+
 Sbjct: 2071 SI 2072

>gi|133594|sp|P26314|RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (ORF1B)
 gi|74826|pir||VFIHB2 genome polyprotein - avian infectious bronchitis
 virus (strain
 Beaudette)
 gi|292953|gb|AAA70234.1| pol protein [Avian infectious bronchitis virus]
 gi|331173|gb|AAA46224.1| ORF1b [Avian infectious bronchitis virus]
 Length = 2652

Score = 570 bits (1469), Expect = e-161

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDEATHACGTNIGTNLPL 1597

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1598 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 1657

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 1658 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1716

171/193

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
Sbjct: 1717 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 1776

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 1777 QDVNWDLTYPHIANEDEVNSSCRYLQRMVYLACVDALKVNVVYDIGNPKGIKCVRRGDVN 1836

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
Sbjct: 1837 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 1893

Query: 365 NLNLPGLDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVP 424
NLPGL+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 1894 VFNLPGLDGGSLYVNKHAFYTPKFDRISEFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 1952

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 1953 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 2012

Query: 485 SL 486
S+
Sbjct: 2013 SI 2014

>gi|29293454|gb|AAO67706.1| ORF1b polyprotein [Avian infectious bronchitis virus]

Length = 2649

Score = 565 bits (1455), Expect = e-160

Identities = 261/482 (54%), Positives = 342/482 (70%), Gaps = 8/482 (1%)

Query: 5 DMTYRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGNTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPL 1597

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GFSTG + V P G +DT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 1598 QVGFSTGADFVVTPEGLIDTSIGNNFEPVNSKAPPGEQFNHLRALFKSAKPWHVIRPRIV 1657

Query: 125 QMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
Sbjct: 1658 QMLADNLCNVSDCVFVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1716

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +G VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DA+MTRCLA++ F
Sbjct: 1717 RHCLG---VYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASADAVMTRCLAINNAFC 1773

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
K V+W ++YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 1774 KDVNWELQYPHIANEDEVNSSCRYLQRMVYLACVDALKVNVVYDIGNPKGIKCVRRGDVN 1833

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y+ H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
Sbjct: 1834 FRFYDKNPIVNVKQFE---YDYSQHKDKFADGLCMFWNCNVDCYPENSLVCRYDTRNLS 1890

172/193

Query: 365 NLNLPGLDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVP 424
NLPGLDGGSLYVNKHAFHTP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 1891 VFNLPGCNGGSLYVNKHAFHTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 1949

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ F+ YNLW F+ LQ
Sbjct: 1950 LATKDCITKCNIGGAVCKKHAQMYAEFVFSYNAAVTAGFTFWVTNNFNPYNLWKNFSALQ 2009

Query: 485 SL 486
S+
Sbjct: 2010 SI 2011

>gi|25121555|ref|NP_740631.1| coronavirus nsp11 [Avian infectious
bronchitis virus]
Length = 521

Score = 559 bits (1440), Expect = e-158
Identities = 261/480 (54%), Positives = 342/480 (71%), Gaps = 5/480 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 47 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPL 106

Query: 65 QLGSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GFSTG+ V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 107 QVGSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 166

Query: 125 QMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
Sbjct: 167 QMLADNLCNVSDCVFVTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 225

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
Sbjct: 226 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 285

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 286 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 345

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNV YP N++VCR+DTR LS
Sbjct: 346 FRFYDKNPVIRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS 402

Query: 365 NLNLPGLDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVP 424
NLPGLDGGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 403 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 461

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 462 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 521

>gi|9635157|ref|NP_058422.1| replicase [Transmissible gastroenteritis
virus]
gi|7801348|emb|CAB91143.1| replicase [Transmissible gastroenteritis virus]

173/193

Length = 6685

Score = 545 bits (1403), Expect = e-153

Identities = 261/484 (53%), Positives = 335/484 (69%), Gaps = 13/484 (2%)

Query: 4 KDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP 63
KD+ Y +IS MGF+ + GY +F TR+ A+R+VRAW+GFDVEG H D VGTN+P
Sbjct: 5574 KDVKYANVISYMGFRFEANIPGYHTLFCTRDFAMRNVRAWLGFDVEGAHVCGDNVGTNP 5633

Query: 64 LQLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKI 123
LQLGFS GV+ V G V TE V A+ PPG+QF HLIPLM KG PW++VR +I
Sbjct: 5634 LQLGFSNGVDFVQTEGCVITEKGNSEVVKARAPPGEQFAHLIPLMRKGQPHIVRRRI 5693

Query: 124 VQMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIG-PERTCCLCDKRATCFSTSSDTYA 182
VQM+ D GLSD ++FVLWA G ELT+M+YFVKIG P++ C C K ATC+S+S YA
Sbjct: 5694 VQMVCDYFDGLSDILIFVLWAGGLELTMMRYFVKIGRPQK--CECGKSATCYSSSQSVYA 5751

Query: 183 CWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHEC 242
C+ H++G DY+YNP+ ID+QQWG+TG+L NH + C +H N HVAS DAIMTRCLA+H+C
Sbjct: 5752 CFKHALGCDYLYNPYCIDIQQWGYTGSLSMNHHEVCNIHRNEHVASGDAIMTRCLAIHDC 5811

Query: 243 FVKRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAE 302
FVKRVDWS+ YP I +E ++N A R VQ V+K+AL +HD+GNPK I+C
Sbjct: 5812 FVKRVDWSIVYPFIDNEEKINKAGRIVQSHVMKAALKIFNPAAIHDVGNPKGIRCA-TTP 5870

Query: 303 VEWKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRV 362
+ W YD P ++ + L Y Y +H +G+ LEWNCNVDP YP +IVCRFDTR
Sbjct: 5871 IPWFCYDRDPINN---NVRCLDYDYMVHGQ--MNLMLFWNCNVDMYPEFSIVCRFDTRT 5925

Query: 363 LSNLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDY 422
S L+L GC+GG+LYVN HAFHTPA+D+ AF LK +PFFYY DS CE V +Y
Sbjct: 5926 RSKLSLEGCGNGGALYVNNHAFHTPAYDRRAFAKLKMPFFYYDDSNC-----LVDGQPNY 5981

Query: 423 VPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTR 482
VPLKS CIT+CN+GGAVC+ HA YR Y++ YN+ + AGF++W + FDTY LW+ F
Sbjct: 5982 VPLKSNVCITKCNIGGAVCKKHAALYRAYVEDYNIFMQAGFTIWCQPQNFDTYMLWHGFVN 6041

Query: 483 LQSL 486
++L
Sbjct: 6042 SKAL 6045

>gi|19387582|ref|NP_598309.1| Pol1 [porcine epidemic diarrhea virus]

gi|13752450|gb|AAK38661.1| Pol1 [porcine epidemic diarrhea virus]

Length = 6781

Score = 541 bits (1394), Expect = e-152

Identities = 256/480 (53%), Positives = 334/480 (69%), Gaps = 12/480 (2%)

Query: 8 YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLG 67
Y +IS MGF+ + + + +F TR+ A+R+VR W+GFDVEG H VGTN+PLQLG
Sbjct: 5675 YEHVISFMGFRFDINIPNHHTLFCTRDFAMRNVRGWLGFDVEGAHVVGSNVGTNPVPLQLG 5734

Query: 68 FSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQML 127
FS GV+ V P G V TE+ V A+ PPG+QF HL+PL+ +G PW+VVR +IVQM
Sbjct: 5735 FSNGVDFVVRPEGCVVTESGDYIKPVRARAPPGEQFAHLLPLLKRGQPWDVVRKRIVQMC 5794

Query: 128 SDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHS 187
 SD L LSD ++FVLWA G ELT+M+YFVKIGP ++C C K ATC++++ TY C+ H+
 Sbjct: 5795 SDYLANLSDILIFVLWAGGLELTTMRYFVKIGPSKSCD-CGKVATCYNALHTYCCFKHA 5853

Query: 188 VGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKRV 247
 +G DY+YNP+ ID+QQWG+ G+L NH +HC VH N HVAS DAIMTRCLA+H+CFVK V
 Sbjct: 5854 LGCDYLYNPYCIDIQQWGYKGSLSLNHHEHCNVHRNEHVASGDAIMTRCLAIHDCFVKNV 5913

Query: 248 DWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEWKF 307
 DWS+ YP IG+E +N + R VQ ++S L ++DIGNPK I+C + +W
 Sbjct: 5914 DWSITYPFIGNEAVINKSGRIVQSHTMRSVLKLYNPKAIYDIGNPKGIRCA-VTDAKWFC 5972

Query: 308 YDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNLN 367
 +D P + +E Y Y I H +F DG+CLFWNCNVD YP ++VCRFDTR S LN
 Sbjct: 5973 FDKNPTNSNVKTLE---YDY-ITHGQF-DGLCLFWNCNVDMYPEFSVVCRFDRCRSPLN 6027

Query: 368 LPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPLKS 427
 L GC+GGSLYVN HAFHTPAFDK AF LK +PFF+Y D+ C+ ++ I+YVPL++
 Sbjct: 6028 LEGCNGGSLYVNNHAFHTPAFDKRAFAKLKPMPPFFFYDDTECD----KLQDSINYVPLRA 6083

Query: 428 ATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFT-RLQSL 486
 + CIT+CN+GGAVC H Y Y++AYN SAGF++W+ FDTYNLW TF+ LQ L
 Sbjct: 6084 SNCITKCNVGGAVCSKHCAMYHSYVNAYNFTTSAGFTIWWPTSFDTYNLWQTFSSNNLQGL 6143

>gi|12175747|ref|NP_073549.1| replicase polyprotein lab [Human coronavirus 229E]

gi|12082740|gb|AAG48591.1|AF304460_2 replicase polyprotein lab [Human coronavirus 229E]:

Length = 6758

Score = 535 bits (1379), Expect = e-151

Identities = 254/478 (53%), Positives = 329/478 (68%), Gaps = 13/478 (2%)

Query: 7 TYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQL 66
 TY +IS MGF+ + + G ++F TR+ A+RHVR W+G DVEG H T D VGTN+PLQ+
 Sbjct: 5642 TYEHVISYMGFRFDVSMPSHSLFCTRDFAMRHVRGWLGMDEGAHVTDGNVGTNVPLQV 5701

Query: 67 GFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQM 126
 GFS GV+ VA P G V T + V A+ PPG+QF H++PL+ KG PW+V+R +IVQM
 Sbjct: 5702 GFSNGVDFVAQPEGCVLTNTGSSVVKPVRARAPPGEQFTHIVPLLRKGQPSVLRKRIVQM 5761

Query: 127 LSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH 186
 ++D L G SD +VFLWA G ELT+M+YFVKIG + C C ATC+++ S+ Y C+ H
 Sbjct: 5762 IADFLAGSSDVLVFLWAGGLELTTMRYFVKIGAVKH-CQCGTVATCYNVSNDYCCFKH 5820

Query: 187 SVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKR 246
 ++G DYVYNP++ID+QQWG+ G+L +NH C VH N HVAS DAIMTRCLAV++CFVK
 Sbjct: 5821 ALGCDYVYNPYVIDIQQWGYVGSLSLNHHAICNVHRNEHVASGDAIMTRCLAVYDCVKN 5880

Query: 247 VDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEWK 306
 VDWS+ YP+I +E +N R VQ ++++A+ +HDIGNPK I+C + +W
 Sbjct: 5881 VDWSITYPMIANENAINKGGRTVQSHIMRAAIKLYNPKAIHDIGNPKGIRCA-VTDAKWY 5939

Query: 307 FYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNL 366

175/193

YD P + +E Y Y H DG+CLFWNCNVD YP +IVCRFDTR S L
 Sbjct: 5940 CYDKNPINSNVKTLE---YDYMTHGQ--MDGLCLFWNCNVDMPYEFSSIVCRFDTRTRSTL 5994

Query: 367 NLPGCDGGSGLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSD-IDYVPL 425
 NL G +GGSGLYVN HAFHTPA+DK A LK PFFYY D CE VV D ++YVPL
 Sbjct: 5995 NLEGVNGGSGLYVNNHAFHTPAYDKRAMAKLKPAPFFYYDDGSCE-----VVHDQVNYVPL 6049

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRL 483
 ++ CIT+CN+GGAVC HAN YR Y+++YN+ AGF++W+ FD YNLW TFT +
 Sbjct: 6050 RATNCITKCNIGGAVCSKHANLYRAYVESYNIFTQAGFNIWVPTTFDCYNLWQTFTEV 6107

>gi|133591|sp|P18458|RRPB_BEV RNA-directed RNA polymerase (ORF1B)
 gi|94017|pir||S11238 polymerase - Berne virus
 gi|1334814|emb|CAA36601.1| 2nd polymerase reading frame (AA 1-2291) [Berne virus]

Length = 2291

Score = 50.1 bits (118), Expect = 8e-05

Identities = 37/103 (35%), Positives = 54/103 (52%), Gaps = 11/103 (10%)

Query: 140 FVLWAHGFELTSMKYFVKIGPERTC--CLCDKRATCFSTSSDTYACWNHSGVF--DYVYN 195
 F+L++ +L S+K++V+ TC C C + A C + Y C N G + N
 Sbjct: 1511 FILYSCSNLKSLLKFYVEFD---TCYFCSCGEMAICLMRDGN-YKCRNCYGGMLISKLVN 1566

Query: 196 PFMIDVQQWGFTGNLQSNHDQHC-QVHGNAHVASCDAIMTRCL 237
 +DVQ+ LQ HD C Q HG++H A CDA+MT+CL
 Sbjct: 1567 CKYLDVQKERV--KLQDAHDAICQQFHHGDSHEALCDAVMTKCL 1607

>gi|1513061|dbj|BAA13323.1| cyanoprotein alpha subunit precursor [Riptortus clavatus]

Length = 693

Score = 34.7 bits (78), Expect = 3.7

Identities = 16/36 (44%), Positives = 22/36 (61%), Gaps = 1/36 (2%)

Query: 371 CDGGSGLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSD 406
 C G LY +KHA P FD+ A+ + Q+P FY+ D
 Sbjct: 643 CGGSKLYDSKHAMGFP-FDRPAYPDAFQVPNFYFKD 677

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

Posted date: Apr 11, 2003 2:30 AM

Number of letters in database: 454,141,287

Number of sequences in database: 1,411,415

| | | |
|--------|-------|-------|
| Lambda | K | H |
| 0.325 | 0.139 | 0.456 |

Gapped

| | | |
|--------|--------|-------|
| Lambda | K | H |
| 0.267 | 0.0410 | 0.140 |

176/193

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 473,361,261
Number of Sequences: 1411415
Number of extensions: 20503315
Number of successful extensions: 51018
Number of sequences better than 10.0: 27
Number of HSP's better than 10.0 without gapping: 26
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 50937
Number of HSP's gapped (non-prelim): 33
length of query: 486
length of database: 454,141,287
effective HSP length: 127
effective length of query: 359
effective length of database: 274,891,582
effective search space: 98686077938
effective search space used: 98686077938
T: 11
A: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 75 (33.5 bits)

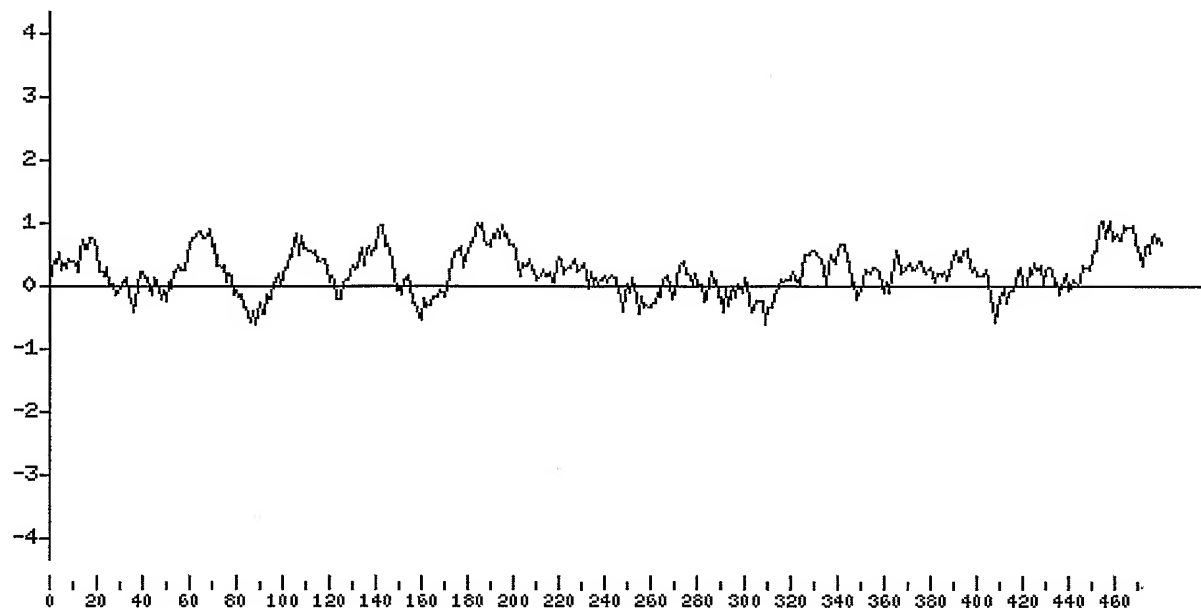
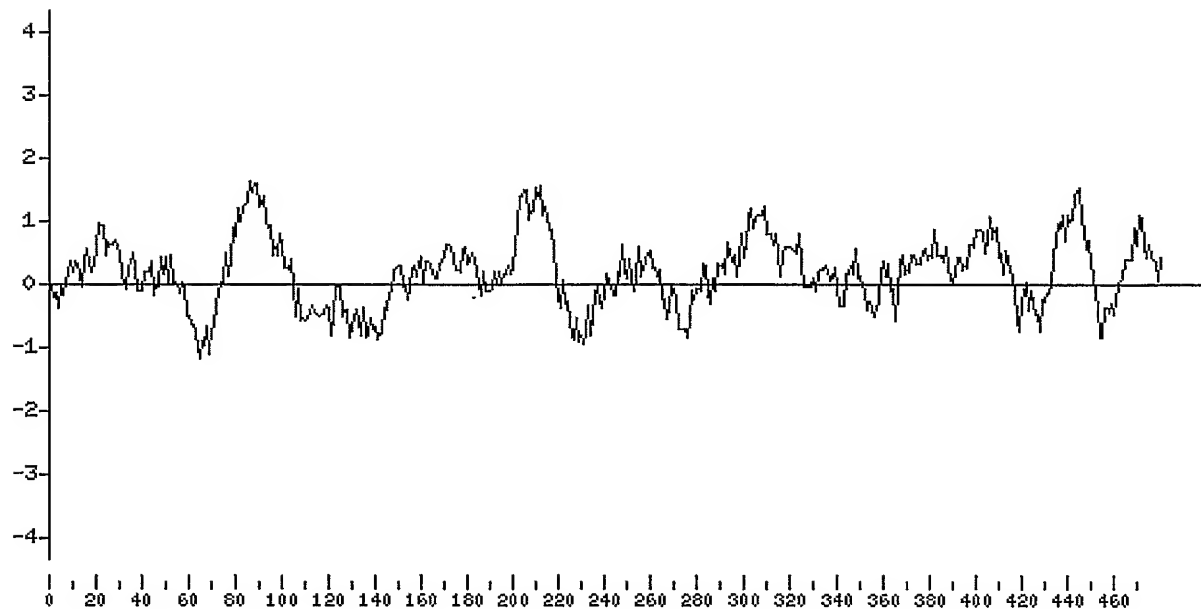
FIGURE 125**FIGURE 125A****FIGURE 125B**

FIGURE 126**5'3' Frame 1**

QVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFHSCFGVRMDMLKPSTQN
YKQVKRGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE--MSQSILNCVNT-IHLL
-LYPPT-ELFTLVL

5'3' Frame 2

RFIKMCVFCD-SFT--LCRDNKVTRFVSDFKSGQGYN-LC-NFIHALV-GWTC-NLLPKT
TSKSSVATRCCDA-LVQDAKNAS-KV-PSELW-KCCYTKRNNDECRKVYSTVSILKYTYF
SCTLQHESYSLWCW

5'3' Frame 3

GSSKCVCSVIDLLLDDFVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVETFYPKL
QASQAWQPGVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMNVAKYTQLCQYLNTLTL
AVPSNMRVIHFGAG

3'5' Frame 1

PAPK-ITLMLEGTAKVSVFKY-HS-VYFATFIIIPFGITAFSP-F-RSHFSRSILCILYK
LGIATPGCHA-LACSFG-KVSTCPSLHQSMNEISA-SIVTLTTFEITDKSCDFIISTKSS
SKRSITEHTHFDEP

3'5' Frame 2

QHQSE-LSCWRVQLK-VYLSIDTVEYTLRHSSLFLLV-QHFHHNSEGHTFQEAFASCTS
-ASQHLVATLDLLVVLGRRFQHVHPYTKA-MKFQHSQ-L-P-PLLKSLTNLVTLLSRQSHQ
VKDQSQNTILMNL

3'5' Frame 3

STKVNNSHVGGYS-SKCI-VLTQLSILCDIHHYSFWYNSIFTIILKVTFLFKKHSLLHVQV
RHRNTWLPRLTCL-FWVEGFNMSILTPKHE-NFSIVNCNLDHF-NH-QIL-LYYLDKVIK
-KINHRTHTF-T

FIGURE 127**5'3' Frame 1**

-VFTYPGKANQPRSLVDLFSKRTN-NV--WTPIKPT-CPPHYIWWTHRFN-Q-PEWRTAM
GQGQNSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPIVVQMTKLATTEELPDE
FVVVTAK-KSSAPDGTSTIT-ELAQKLHFPTALTKKASYGLQLREP-IHPKTTLAPAILIT
MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQLLAAGVEILLLEWLAE
VVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKSLAKNVLPQNSTTSLKH
LGDVVQNKPKESGTKT-SDKELITNIGPQIAQFA

5'3' Frame 2

RFLPTQEKPTNLDLL-ICSLNEQIKMSDNGPQSNQORSAPRITFGGPTDSTDNNQNGGLQW
GKAKTAPTPTFTQ-YCVLVHSSHSWQGGT-IPSRPGRSNQHQ-WSR-PNWLLPKSYPTS
SWW-RQNERAQPQMVLLLPRNWPRSFTSLRR-QRRHRMGCN-GSLEYTQRPHWHPQS--Q
CCHRAATSSRNIAKRLLRGKQRRQSSSLFSLIT-SR-FKKFNSWQQ-GKFSCSNG-RR
W-NCPRAIARQIEPA-EQSFW-RPTTTRPNCH-EICC-GI-KASPKTYCHKTVQRHSSI
WETWSRTNPRKFRGPRPNQTRN-LQTLGRKLHNLP

5'3' Frame 3

GFYLPRKSQPTSISCRSVL-TNKLKCLIMDPNQTNVVPPALHLVDPQIQLTITRMEDCNG
ARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRATRVR
RGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN
AATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGG
GETALALLLLDRLNQLESKVSQKQGGQGGQTVTKKSAAEASKKPRQKRTATKQYNVTQAF
GRRGPEQTQGNFGDQDLIRQGTQDYKHWAANCTIC

3'5' Frame 1

RQIVQFAAQCL-SVPCLIRSWSPKFPWVCSGPRLPNA-VTLYCFVAVRFWRGFLDASAAD
FLVTWVPCCWPLPETLLSSWFNLSSSNSARAVSPPLAIRAGEFPLLLPGVEFLELPRL
RDEEREEA-LPPLLPSA-KPFGNVVP-GSCSTVAALLLGLRVPMWSLGVFKAPSVATHM
PSLLAP-GSEASGPVPR--KYHLGLSSFILPSPPRTRRVALR--PIWSSGPLLVLIGTPW
PRGNLSSSLPC-VRAVNQDAILLGKPWGRRCFGLAPLQSSILVIVS-ICGSTKCNAGGTT
LV-LGSIIRHFNLFV-RTDLQEIEVGWFLGR-KP

3'5' Frame 2

GKLCNLRPNVCNQFLV-LGLGPRNFLGFVLDHVSQMLE-RCTVLWQYVFGGEAF-MPQQQI

S--QFGLVVVGLYQKLC SQAGSICLAAIARGQFHHLR-PFEQENFPYCCQELNFLNYR DY
 VMRSEKRLDCRLCFPLRRSLLAMLFL EEFVARWQH CY-DCGCQCGLWVYSRLPQLQPIRC
 LLC-RRREVKLLGQFLGNRSTIWG-ALSF CRHHHEL VG-LFGSSQFGHLDHYWC-LERPG
 LEGI-VPPCHAE-EL-TKTQYYWVNLGVGAVLALPHCSPPFWLLSVESVGPPNVMRGALR
 WFDWGPLSDILICSFREQIYKRSRLVGFSWVGKNL

3'5' Frame 3

ANCAICGPMFVISSLSD-VLVPEISLGLFWTTSPKCLSDVVLFCGSTFLARLFRCLSSRF
 LSDSLALLLLAFTRNFALKLVQSV-QQ-REGSFTTSASHSSRRISPTAARS-IS-ITATT
 --GARRGLTAASASLCVEAFWQCCSLRKL-HGGSIVIRIAGANVVF GCIQGSLS CNPYDA
 FFVSAVGK-SFWASS-VIEVPSGAELFHFAVTTTNSSGSSSVVANLVIWTTIGVDWNALA
 SRESKFL LAMLESECEPRNIIG-TLGSALFWPCPIAVLHSGYCQLNLVWHQM-CGGHYV
 GLIGVHYQTF-FVRLNRSTRDRGWLA FPG-VKT

FIGURE 128

-GLELKL-LTSICAF-PFCYSLF--CLLYFGFH SKSRI-KNLVPKSKRT-NFSLF-LVFL
 YAVAYAL-YSAVHLINLMCLKILVRYNTRGNTYSTAWLCALGKVL PFHRWHTMVQTCTPN
 VTINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN-NV--WTPIKPT-CPPHYI
 WWTHRFN-Q-PEWRTQWGKAKTAPT PRFTQ-YCVLVHSSHS AWQGGT-IPSRPGRSNQHQ
 -WSR-PNWLLPKSYPTSSWW-RQNERAQPQMVLLLPRNWPRSFTSLRR-QRRHRMGCN-G
 SLEYTQRPHWHPQS--QCCHRATTSSRN NIAKRLLRGKQRRQSSLFSLIT-SR-FKKF
 NSWQQ-GKFSCSNG-RRW-NCPRAI AARQIEPA-EQSFWRPTTTRPNCH-EICC-GI-K
 ASPKTYCHKTVQRHSSIWETWSRTNPRKFRGPRPNQTRN-LQTLAANCTICSKCLCILWN
 VTHWHGSHTFGNMADLSWSH-IG-QRSTIQRQRHTAEQAH-RIQNIPTNRA-KGQKEKD-
 -SSAFAAETKEAAHCDSSSC

EDSSSSFN-LLFVLFSLSAIPCFNNAYYILVFTRNPGSRRTLYQSLNEHETSHCFDLYFS
 MQLHMH CSTALCI--TSCA-RSL-GTTLGVILIALLG FVL-ERFYLFIDGTLWFKHAHLM
 LLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLLF-INEQIKMSDNGPQSNQRSAPRITF
 GGPTDSTDNNQNGGRNGARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPI NTN
 SGPDDQIGYYRRATRVRGGDGKMKELSPRWYFY YLGTGPEASLPYGANKEGIVWVATEG
 ALNTPKDHIGTRNPNNNAATVLQLPQGTTL PKGFYAEGSRGGSQASSRSSSRSGNSRNS
 TPGSSRGNSPARMASGGGETALALLLDRLNQLESKVS GKGQQQQGQTVTKKSAAEASKK
 PRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGT DYKHWPOIAQFAPSASAFFGM
 SRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFPPTPEPKDKKKKTD
 EAQPLPQRQKKQPTVTLLP

RTRAQALIDFYLCFLAFLFLVLIMLIIFWFSLEIQDLEEPCTKV-TNMKLLIVLTCISL
CSCICTVVQRCASNKPHVLEDPCVKQH-G-YL-HCLALCSRKGFTFS-MAHYGSNMHT-C
YYQLSRSSWWCAYS-VLVPS-RSPNCCI-RRTCCFK-TNKLKCLIMDPNQTNVVPPALHL
VDPQIQLTITRMEAMGQONSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPI
VVQMTKLATTEELPDEFVVVTAK-KSSAPDGTST-ELAQKLHFPTALTKKASYGLQIRE
P-IHPKTTLAPAILITMLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQ
LLAAVGEILLLEWLAEVVKLPSRYCC-TD-TSLRAKFLVKANNNKAKLSLRNLLLRHLKS
LAKNVLPQNSTTSLKHLGDVVQNKPKKEISGTKT-SDKELITNIGRKLHNLLQVPLHSLEC
HALAWKSHLREHG-LIMEPLNWMTKIHNSKTTSYC-TSTLTHTKHSQQSLKRTKRKRLM
KLSLCRRDKRSSPL-LFFL

FIGURE 129

5'3' Frame 1

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttaccct
Y R R L I S M M G F K M N Y Q V N G Y P
aatatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgat
N M F I T R E E A I R H V R A W I G F D
gtagagggtgtcatgcaactagagatgctgtgggtactaacctacctctccagctagga
V E G C H A T R D A V G T N L P L Q L G
tttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataac
F S T G V N L V A V P T G Y V D T E N N
acagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
T E F T R V N A K P P P G D Q F K H L I

5'3' Frame 2

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttacccta
T V D S S L - W V S K - I T K S M V T L
atatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgatg
I C L S P A K K L F V T F V R G L A L M
tagagggtgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggat
- R A V M Q L E M L W V L T Y L S S - D
tttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataaca
F L Q V L T - - L Y R L V M L T L K I T
cagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
Q N S P E L M Q N L H Q V T S L N I L Y

5'3' Frame 3

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttaccctaa
P - T H L Y D G F Q N E L P S Q W L P -
tatgtttatcacccgcgaagaagctatttcgtcacggttcgtgcggtggattggctttgatgt
Y V Y H P R R S Y S S R S C V D W L - C
agagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggatt
R G L S C N - R C C G Y - P T S P A R I
ttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataacac
F Y R C - L S S C T D W L C - H - K - H
agaattcaccagaggttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
R I H Q S - C K T S T R - P V - T S Y T

3'5' Frame 1

ggtataagatgttttaaactgggtcacctgggtggagggttttgcattaactctggtgaattct
G I R C L N W S P G G G F A L T L V N S
gtgttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaa
V L F S V S T - P V G T A T K L T P V E
aatcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctct
N P S W R G R L V P T A S L V A - Q P S
acatcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacata
T S K P I H A R T - R I A S S R V I N I
ttagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
L G - P L T W - F I L K P I I E M S L R

3'5' Frame 2

ggtataagatgttttaaactgggtcacctgggtggagggttttgcattaactctggtgaattctg
V - D V - T G H L V E V L H - L W - I L
tggtatttttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaa
C Y F Q C Q H N Q S V Q L L S - H L - K
atcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctcta
I L A G E V G - Y P Q H L - L H D S P L
catcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatat
H Q S Q S T H E R D E - L L R G - - T Y
tagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
- G N H - L G N S F - N P S - R - V Y G

3'5' Frame 3

ggtataagatgtttaaactgggtcacctgggtggaggttttgcattaactctgggtgaattctgt
Y K M F K L V T W W R F C I N S G E F C
gttatttttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaa
V I F S V N I T S R Y S Y - V N T C R K
tcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctac
S - L E R - V S T H S I S S C M T A L Y
atcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatatt
I K A N P R T N V T N S F F A G D K H I
agggtaaccattgacttggtaattcattttgaaacccatcatagagatgagtctacggta
R V T I D L V I H F E T H H R D E S T V

FIGURE 130

| | 10 | 20 | 30 | 40 | 50 | 60 |
|-----------------|--|--------------------|------|----|----|----|
| SEQ ID NO: 9997 | KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVR | AWIGFDVEGCHATRDAVG | TNLP | | | |
| SEQ ID NO:10034 | ----YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVR | AWIGFDVEGCHATRDAVG | TNLP | | | |
| Prim. Cons. | KGHD2RRLISMMGFKMNYQVNGYPNMFITREEAIRHVR | AWIGFDVEGCHATRDAVG | TNLP | | | |

| | 70 | 80 | 90 | 100 | 110 | 120 |
|-----------------|---|------|----|-----|-----|-----|
| SEQ ID NO: 9997 | LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNV | RIKI | | | | |
| SEQ ID NO:10034 | LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAKPPPGDQFKHLI----- | | | | | |
| Prim. cons. | LQLGFSTGVNLVAVPTGYVDTENNT2FTRVNA22222QFKHLIPLMYKGLPWNV | RIKI | | | | |

| | 130 | 140 | 150 | 160 | 170 | 180 |
|-----------------|---|------|-----|-----|-----|-----|
| SEQ ID NO: 9997 | VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD | TYAC | | | | |
| SEQ ID NO:10034 | ----- | | | | | |
| Prim. cons. | VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD | TYAC | | | | |

| | 190 | 200 |
|-----------------|----------------------------|-----|
| SEQ ID NO: 9997 | WNHSVGFQDYVYNPFMIDVQQWGLYG | |
| SEQ ID NO:10034 | ----- | |

FIGURE 131**5'3' Frame 1**

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgaga
Q V H Q N V C V L - L I F Y L M T L S R
taataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatg
- - S H K I C Q - F Q K W S R L Q L T M
ctgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaac
L K F H S C F G V R M D M L K P S T Q N
tacaagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaa
Y K Q V K R G N Q V L R C L T C T R C K
gaatgcttcttgaaaagtggtgaccttcagaattatggtgaaaatgctgttataccaaaag
E C F L K S V T F R I M V K M L L Y Q K
gaataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaaatacacttactt
E - - - M S Q S I L N C V N T - I H L L
tagctgtaccctccaacatgagagttattcactttggtgctgg
- L Y P P T - E L F T L V L

5'3' Frame 2

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagat
R F I K M C V F C D - S F T - - L C R D
aataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatgc
N K V T R F V S D F K S G Q G Y N - L C
tgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaact
- N F I H A L V - G W T C - N L L P K T
acaagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaag
T S K S S V A T R C C D A - L V Q D A K
aatgcttcttgaaaagtggtgaccttcagaattatggtgaaaatgctgttataccaaaagg
N A S - K V - P S E L W - K C C Y T K R
aataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaaatacacttacttt
N N D E C R K V Y S T V S I L K Y T Y F
agctgtaccctccaacatgagagttattcactttggtgctgg
S C T L Q H E S Y S L W C W

5'3' Frame 3

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagata
G S S K C V C S V I D L L L D D F V E I
ataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatgct
I K S Q D L S V I S K V V K V T I D Y A
gaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaacta
E I S F M L W C K D G H V E T F Y P K L
caagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaaga

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Q A S Q A W Q P G V A M P N L Y K M Q R
atgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttataccaaaaagga
M L L E K C D L Q N Y G E N A V I P K G
ataatgatgaatgtcgcgaaagtataactcaactgtgtcaataacttaaatacacttacttta
I M M N V A K Y T Q L C Q Y L N T L T L
gctgtaccctccaacatgagaggttattcacttttggtgctgg
A V P S N M R V I H F G A

3'5' Frame 1

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaag
P A P K - I T L M L E G T A K V S V F K
tattgacacagttgagtatactttgcgacattcatcattattccttttgggtataaacagca
Y - H S - V Y F A T F I I I P F G I T A
ttttcaccataatttctgaagggtcacacttttcaagaagcattcctttgcatccttgtaacaag
F S P - F - R S H F S R S I L C I L Y K
ttaggcacgcgaacacctgggttgccacgcttgacttgcttgtagttttgggtagaagggtt
L G I A T P G C H A - L A C S F G - K V
tcaacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacc
S T C P S L H Q S M N E I S A - S I V T
ttgaccacttttgaaatcactgacaaatccttggtgactttattatctcgacaaagtcatca
L T T F E I T D K S C D F I I S T K S S
agtaaaagatcaatcacagaacacacacattttgatgaacctg
S K R S I T E H T H F D E P

3'5' Frame 2

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaagt
Q H Q S E - L S C W R V Q L K - V Y L S
attgacacagttgagtatactttgcgacattcatcattattccttttgggtataaacagcat
I D T V E Y T L R H S S L F L L V - Q H
tttcaccataatttctgaagggtcacacttttcaagaagcattcctttgcatccttgtaacaag
F H H N S E G H T F Q E A F F A S C T S
taggcacgcgaacacctgggttgccacgcttgacttgcttgtagttttgggtagaagggtt
- A S Q H L V A T L D L L V V L G R R F
caacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacct
Q H V H P Y T K A - M K F Q H S Q L - P
tgaccacttttgaaatcactgacaaatccttggtgactttattatctcgacaaagtcatcaa
- P L L K S L T N L V T L L S R Q S H Q
gtaaaagatcaatcacagaacacacacattttgatgaacctg
V K D Q S Q N T H I L M N L

3'5' Frame 3

ccagcaccaaagtgaataactctcatgttgagggtacagctaaagtaagtgtattttaagta
 S T K V N N S H V G G Y S - S K C I - V
 ttgacacagttgagtatacttttgcgacattcatcattattccttttgggtataacagcatt
 L T Q L S I L C D I H H Y S F W Y N S I
 ttcaccataattctgaagggtcacactttttcaagaagcattcctttgcatcttgtacaagtt
 F T I I L K V T L F K K H S L H L V Q V
 aggcacgcgaacacctggttgccacgcttgacttgcttgtagttttgggtagaaggtttc
 R H R N T W L P R L T C L - F W V E G F
 aacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcattgtaacctt
 N M S I L T P K H E - N F S I V N C N L
 gaccacttttgaaatcactgacaaatcctgtgacttttattatctcgacaaagtcacaaag
 D H F - N H - Q I L - L Y Y L D K V I K
 taaaagatcaatcacagaacacacacattttgatgaacctg
 - K I N H R T H T F - - T

FIGURE 132

5'3' Frame 1

taggtttttacctacccaggaaaagccaaccaacctcgatctctttagatctgttctct
 - V F T Y P G K A N Q P R S L V D L F S
 aaacgaacaaattaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccg
 K R T N - N V - - W T P I K P T - C P P
 cattacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatg
 H Y I W W T H R F N - Q - P E W R T A M
 gggcaaggccaaaacagcgccgaccccaagggtttaccaataatattgcgtcttgggttca
 G Q G Q N S A D P K V Y P I I L R L G S
 cagctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggttccaa
 Q L S L S M A R R N L D S L E A R A F Q
 tcaacaccaatagtggtccagatgaccaaattggctactaccgaagagctacccgacgag
 S T P I V V Q M T K L A T T E E L P D E
 ttcgtgggtggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctag
 F V V V T A K - K S S A P D G T S I T -
 gaactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgatgggttg
 E L A Q K L H F P T A L T K K A S Y G L
 caactgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataaca
 Q L R E P - I H P K T T L A P A I L I T
 atgctgccaccgtgctacaacttctcaaggaacaacattgccaaaaggcttctacgcag
 M L P P C Y N F L K E Q H C Q K A S T Q
 agggaagcagaggcggcagtcagcctcttctcgtcctcatcacgtagtcgcggtaatt
 R E A E A A V K P L L A P H H V V A V I
 caagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggag
 Q E I Q L L A A V G E I L L L E W L A E

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gtggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaag
V V K L P S R Y C C - T D - T S L R A K
tttctggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgagg
F L V K A N N N K A K L S L R N L L L R
catctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcat
H L K S L A K N V L P Q N S T T S L K H
ttgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagac
L G D V V Q N K P K E I S G T K T - S D
aaggaactgattacaaacattggggccgcaaattgcacaatttgcct
K E L I T N I G P Q I A Q F A

5'3' Frame 2

taggtttttacctaccaggaagccaaccaacctcgatctctttagatctgttctcta
R F L P T Q E K P T N L D L L - I C S L
aacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgtccccgc
N E Q I K M S D N G P Q S N Q R S A P R
attacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatgg
I T F G G P T D S T D N N Q N G G L Q W
ggcaaggccaaaacagcgccgacccaagggtttaccaataatattgcgtcttggttcac
G K A K T A P T P R F T Q - Y C V L V H
agctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcgttccaat
S S H S A W Q G G T - I P S R P G R S N
caacaccaatagtgggtccagatgaccaaattgggtactaccgaagagctacccgacgagt
Q H Q - W S R - P N W L L P K S Y P T S
tcgtgggtgggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctagg
S W W - R Q N E R A Q P Q M V L L L P R
aactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtatgggttgc
N W P R S F T S L R R - Q R R H R M G C
aactgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaa
N - G S L E Y T Q R P H W H P Q S - - Q
tgctgccaccgtgctacaacttcctcaaggaacaacattgccaaaaggcttctacgcaga
C C H R A T T S S R N N I A K R L L R R
gggaagcagaggcggcagtcagcctcttctcgtcctcatcacgtagtcgcggtaatc
G K Q R R Q S S L F S L L I T - S R - F
aagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggagg
K K F N S W Q Q - G K F S C S N G - R R
tggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagt
W - N C P R A I A A R Q I E P A - E Q S
ttctggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggc
F W - R P T T T R P N C H - E I C C - G
atctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcatt
I - K A S P K T Y C H K T V Q R H S S I
tgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagaca
W E T W S R T N P R K F R G P R P N Q T
aggaactgattacaaacattggggccgcaaattgcacaatttgcct
R N - L Q T L G R K L H N L P

5'3' Frame 3

taggttttttacctacccaggaaaagccaaccaacctcgatctctttagatctgttctctaa
G F Y L P R K S Q P T S I S C R S V L -
acgaacaaattaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccgca
T N K L K C L I M D P N Q T N V V P P A
ttacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatggg
L H L V D P Q I Q L T I T R M E D C N G
gcaaggccaaaacagcgccgaccccaagggtttacccaataatattgcttcttggttcaca
A R P K Q R R P Q G L P N N I A S W F T
gctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcggttccaatc
A L T Q H G K E E L R F P R G Q G V P I
aacaccaatagtgggtccagatgaccaaattggctactaccgaagagctacccgacgagtt
N T N S G P D D Q I G Y Y R R A T R R V
cgtgggtggtagcggcaaaatgaaagagctcagccccagatgggtacttctattacctagga
R G G D G K M K E L S P R W Y F Y Y L G
actggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtaggggttga
T G P E A S L P Y G A N K E G I V W V A
actgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaat
T E G A L N T P K D H I G T R N P N N N
gctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcagag
A A T V L Q L P Q G T T L P K G F Y A E
ggaagcagaggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggttaattca
G S R G G S Q A S S R S S S R S R G N S
agaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggaggt
R N S T P G S S R G N S P A R M A S G G
ggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagtt
G E T A L A L L L L D R L N Q L E S K V
tctggttaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggca
S G K G Q Q Q Q G Q T V T K K S A A E A
tctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcattt
S K K P R Q K R T A T K Q Y N V T Q A F
gggagacgtgggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagacaa
G R R G P E Q T Q G N F G D Q D L I R Q
ggaactgattacaaacattgggcccgaattgcacaatttgcct
G T D Y K H W A A N C T I C

3'5' Frame 1

aggcaaatgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtct
R Q I V Q F A A Q C L - S V P C L I R S
tggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaattgcttgagtgcg
W S P K F P W V C S G P R L P N A - V T
ttgtactgttttggcagtagcttttggcgaggctttttagatgcctcagcagcagat

L Y C F V A V R F W R G F L D A S A A D
ttcttagtgacagtttggccttggtgttggtggcctttaccagaaactttgctctcaagc
F L V T V W P C C C W P L P E T L L S S
tggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccatt
W F N L S S S N S A R A V S P P P L A I
cgagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgacta
R A G E F P L L L P G V E F L E L P R L
cgtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcct
R D E E R E E A - L P P L L P S A - K P
tttggcaatgttggttcccttgaggaagttgtagcacggtggcagcattgttattaggattg
F G N V V P - G S C S T V A A L L L G L
cgggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacgatg
R V P M W S L G V F K A P S V A T H T M
ccttctttgttagcgccgtagggaagtgaagcttctgggccagttccttaggtaatagaag
P S L L A P - G S E A S G P V P R - - K
taccatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagct
Y H L G L S S F I L P S P P R T R R V A
cttcggtagtagccaatttggtcatctggaccactattggtgttgattggaacgccctgg
L R - - P I W S S G P L L V L I G T P W
cctcgaggggaatctaagttcctccttgccatgctgagtgaagacgca
P R G N L S S S L P C - V R A V N Q D A
atattattgggttaaacccttggggtcggcgctgttttggccttgccccattgcagtcctcc
I L L G K P W G R R C F G L A P L Q S S
attctggttattgtcagttgaatctgtgggtccaccaaataatgacggggggcactacg
I L V I V S - I C G S T K C N A G G T T
ttggtttgattgggggtccattatcagacatttttaatttggttcgtttagagaacagatcta
L V - L G S I I R H F N L F V - R T D L
caagagatcgaggttggttggttttccctgggtaggtaaaaaccta
Q E I E V G W L F L G R - K P

3'5' Frame 2

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtctt
G K L C N L R P N V C N Q F L V - L G L
gggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaatagttgagtacgt
G P R N F L G F V L D H V S Q M L E - R
tgtactgttttgtggcagtagcttttggcgaggcttttttagatgcctcagcagcagatt
C T V L W Q Y V F G E A F - M P Q Q Q I
tcttagtgacagtttggccttggtgttggtggcctttaccagaaactttgctctcaagct
S - - Q F G L V V V G L Y Q K L C S Q A
gggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattc
G S I C L A A I A R G Q F H H L R - P F
gagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactac
E Q E N F P Y C C Q E L N F L N Y R D Y
gtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcctt
V M R S E K R L D C R L C F P L R R S L
ttggcaatgttggttcccttgaggaagttgtagcacggtggcagcattgttattaggattgc

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L A M L F L E E V V A R W Q H C Y - D C
gggtgccaatgtggtcctttgggtgtattcaaggctccctcagttgcaacccatacgatgc
G C Q C G L W V Y S R L P Q L Q P I R C
cttctttgttagcgccgtaggggaagtgaagcttctgggccagttcctaggtaatagaagt
L L C - R R R E V K L L G Q F L G N R S
accatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagctc
T I W G - A L S F C R H H H E L V G - L
ttcggtagtagccaatttgggtcatctggaccactattggtggttgattggaacgccctggc
F G S S Q F G H L D H Y W C - L E R P G
ctcgaggggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaa
L E G I - V P P C H A E - E L - T K T Q
tattattgggtaaaccttggggctcggcgctgttttggccttgccccattgcagtcctcca
Y Y W V N L G V G A V L A L P H C S P P
ttctggttattgtcagttgaatctgtgggtccaccaaataatgtaatgcggggggcactacgt
F W L L S V E S V G P P N V M R G A L R
tggtttgattgggggtccattatcagacattttaatttgttcgtttagagaacagatctac
W F D W G P L S D I L I C S F R E Q I Y
aagagatcgaggttggttggccttttctgggtaggtaaaaaccta
K R S R L V G F S W V G K N L

3'5' Frame 3

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtcttg
A N C A I C G P M F V I S S L S D - V L
gtccccgaaatttcccttgggtttgttctggaccacgtctcccaaatagtttgagtgacgtt
V P E I S L G L F W T T S P K C L S D V
gtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagattt
V L F C G S T F L A R L F R C L S S R F
cttagtgacagtttggccttgttgttggcctttaccagaaactttgctctcaagctg
L S D S L A L L L L A F T R N F A L K L
gttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattcg
V Q S V - Q Q - R E G S F T T S A S H S
agcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactacg
S R R I S P T A A R S - I S - I T A T T
tgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagccttt
- - G A R R G L T A A S A S L C V E A F
tggcaatgttggtccttgaggaagttgtagcacggtggcagcattgttattaggattgcg
W Q C C S L R K L - H G G S I V I R I A
ggtgccaatgtggtcctttgggtgtattcaaggctccctcagttgcaacccatacgatgcc
G A N V V F G C I Q G S L S C N P Y D A
ttctttgttagcgccgtaggggaagtgaagcttctgggccagttcctaggtaatagaagta
F F V S A V G K - S F W A S S - V I E V
ccatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagctct
P S G A E L F H F A V T T T N S S G S S
tcggtagtagccaatttgggtcatctggaccactattggtggttgattggaacgccctggcc
S V V A N L V I W T T I G V D W N A L A
tcgaggggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaat

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S R E S K F L L A M L S E S C E P R R N
attattgggtaaacccttgggggtcggcgctgttttggccttgccccattgcagtcctccat
I I G - T L G S A L F W P C P I A V L H
tctgggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgtt
S G Y C Q L N L W V H Q M - C G G H Y V
ggtttgattgggggtccattatcagacattttaatttggttcgtttagagaacagatctaca
G L I G V H Y Q T F - F V R L E N R S T
agagatcgaggttgggttggttttctgggtaggtaaaaaccta
R D R G W L A F P G - V K T

FIGURE 133

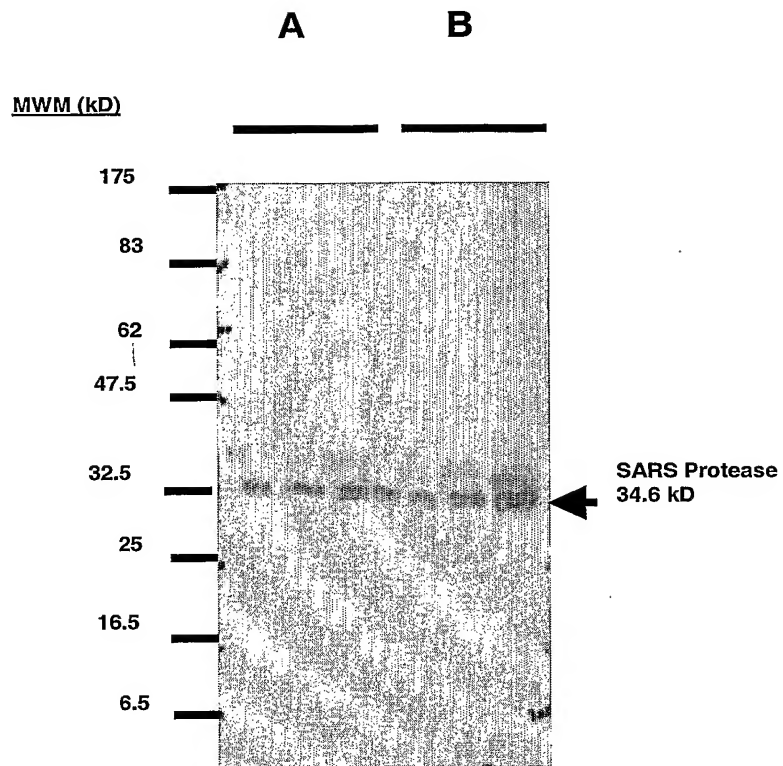


FIGURE 134